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**Guerry et al.**

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- (54) **COMBINED ENTEROPATHOGEN RECOMBINANT CONSTRUCT**
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**Related U.S. Application Data**

- (63) Continuation-in-part of application No. 11/340,003, filed on Jan. 10, 2006, now Pat. No. 9,079,945, and a continuation-in-part of application No. 11/524,057, filed on Sep. 20, 2006, now Pat. No. 9,084,809, and a continuation-in-part of application No. 14/048,264, filed on Oct. 8, 2013, now Pat. No. 9,328,150.
- (60) Provisional application No. 60/642,771, filed on Jan. 11, 2005, provisional application No. 62/075,399, filed on Nov. 5, 2014, provisional application No. 62/034,436, filed on Aug. 7, 2014, provisional application No. 60/722,086, filed on Sep. 21, 2005, provisional application No. 62/054,454, filed on Sep. 24, 2014, provisional application No. 62/127,927, filed on Mar. 4, 2015, provisional application No. 62/165,301, filed on May 22, 2015, provisional application No. 61/727,943, filed on Nov. 19, 2012, provisional application No. 62/127,935, filed on Mar. 4, 2015.

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**A61K 39/02** (2006.01)  
**A61K 39/385** (2006.01)  
**A61K 39/108** (2006.01)

- A61K 47/64** (2017.01)  
**C07K 16/12** (2006.01)  
**A61K 39/112** (2006.01)  
**C07K 16/44** (2006.01)  
**A61K 39/00** (2006.01)

- (52) **U.S. Cl.**  
 CPC ..... **A61K 47/646** (2017.08); **A61K 39/0258** (2013.01); **A61K 39/0283** (2013.01); **A61K 39/105** (2013.01); **A61K 47/6415** (2017.08); **C07K 14/245** (2013.01); **C07K 16/1232** (2013.01); **C07K 16/1267** (2013.01); **C07K 16/44** (2013.01); **A61K 39/00** (2013.01); **A61K 2039/55505** (2013.01); **A61K 2039/6037** (2013.01); **A61K 2039/70** (2013.01); **C07K 2317/55** (2013.01); **C07K 2317/76** (2013.01); **C07K 2319/35** (2013.01); **Y02A 50/47** (2018.01); **Y02A 50/474** (2018.01); **Y02A 50/476** (2018.01)

- (58) **Field of Classification Search**  
 CPC . **A61K 47/646**; **A61K 39/0258**; **A61K 39/105**  
 See application file for complete search history.

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(57) **ABSTRACT**

The inventive subject matter relates to a construct comprising antigens derived from multiple enterobacteria including *Campylobacter jejuni* capsule polysaccharide polymer, enterotoxigenic *Escherichia coli* recombinant polypeptide construct and lipopolysaccharide from *Shigella* spp. The subject invention also relates to a method of inducing an immune response utilizing the inventive composition.

**20 Claims, 12 Drawing Sheets**  
**Specification includes a Sequence Listing.**

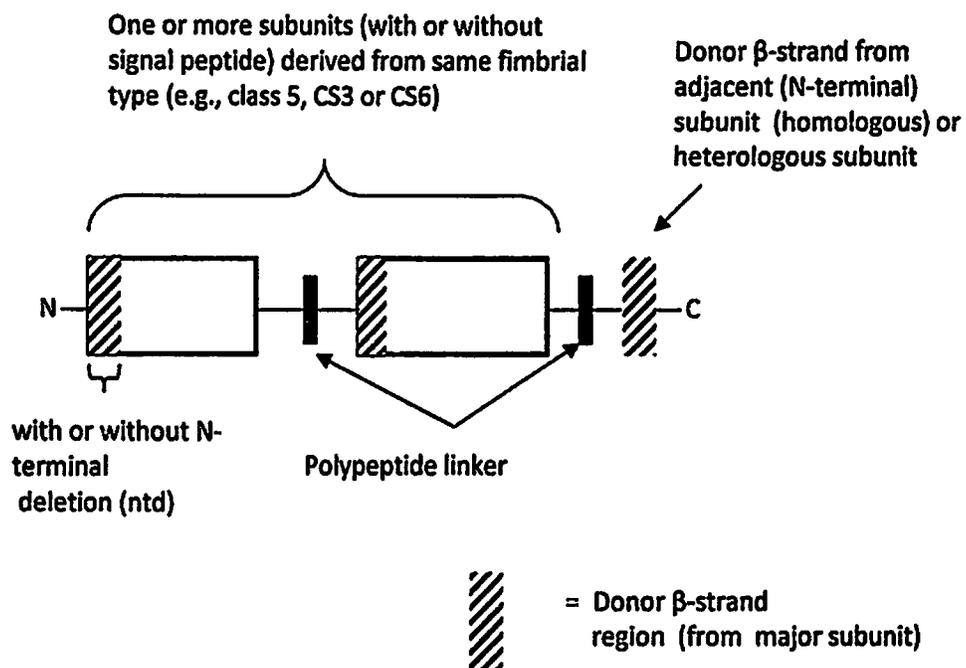


FIG. 1

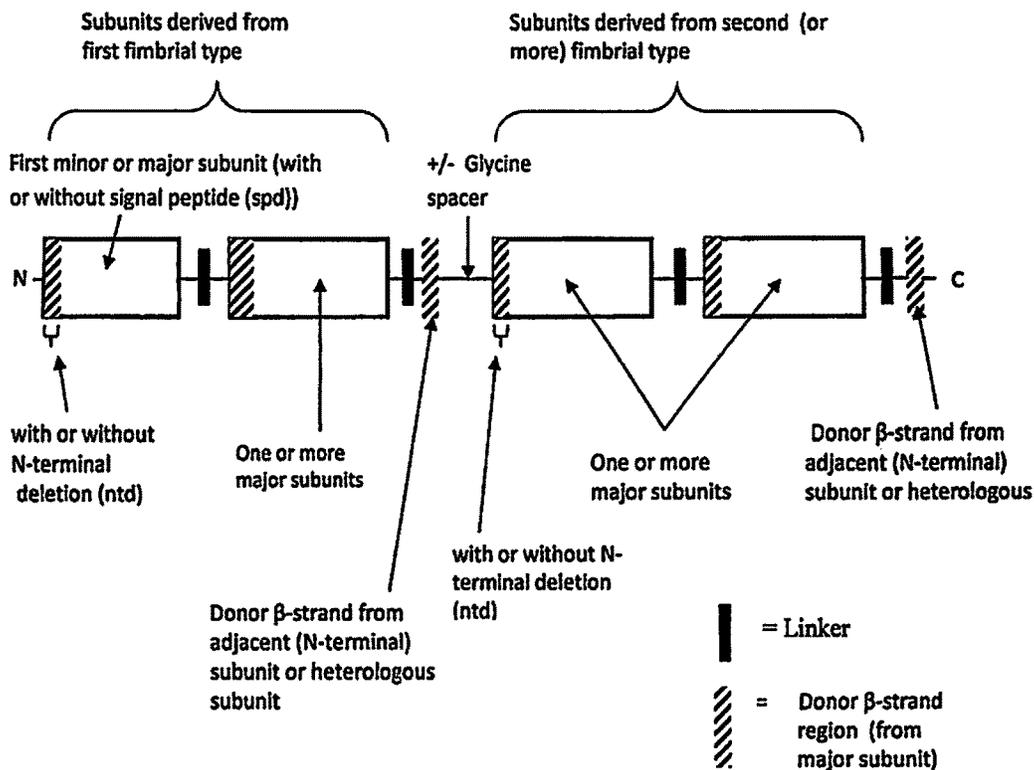


FIG. 2

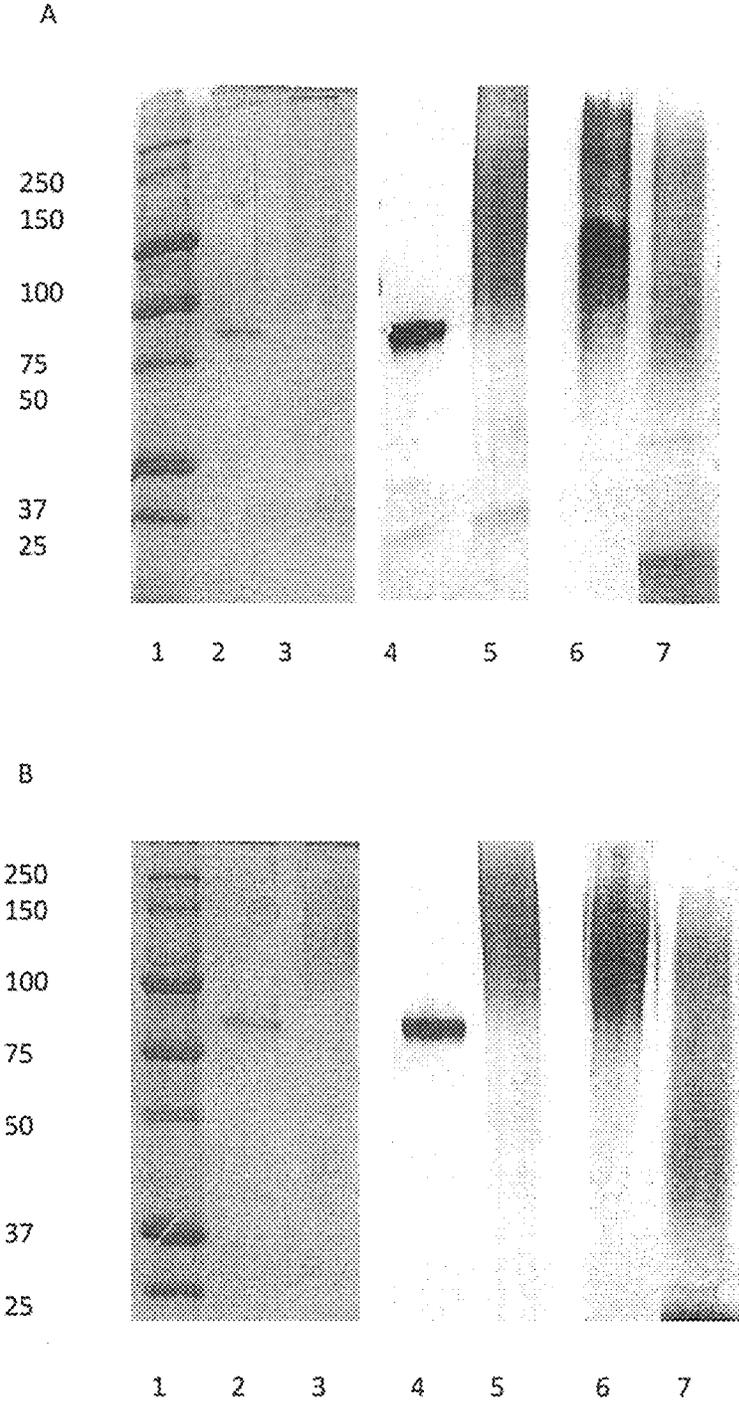


FIG. 3

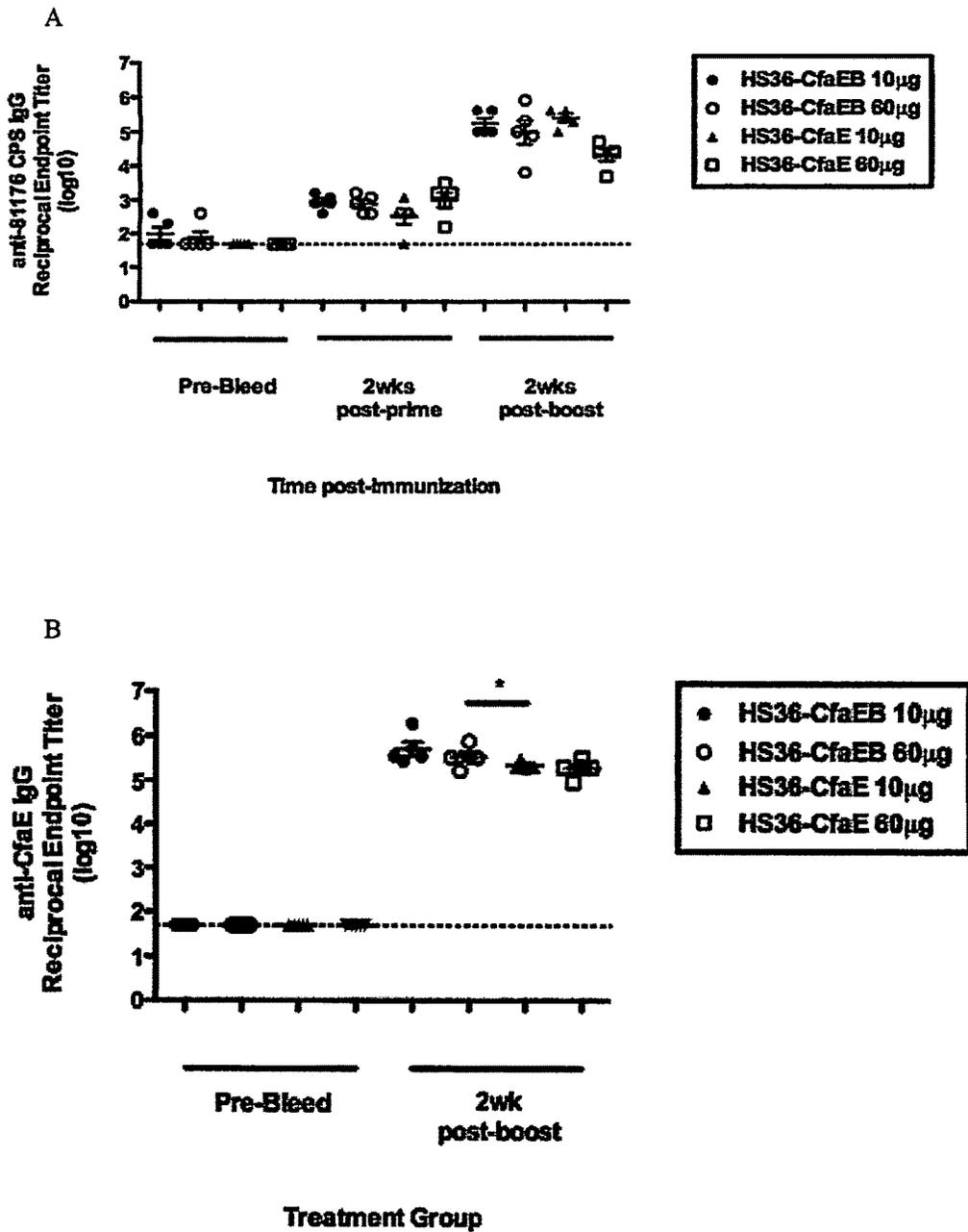


FIG. 4

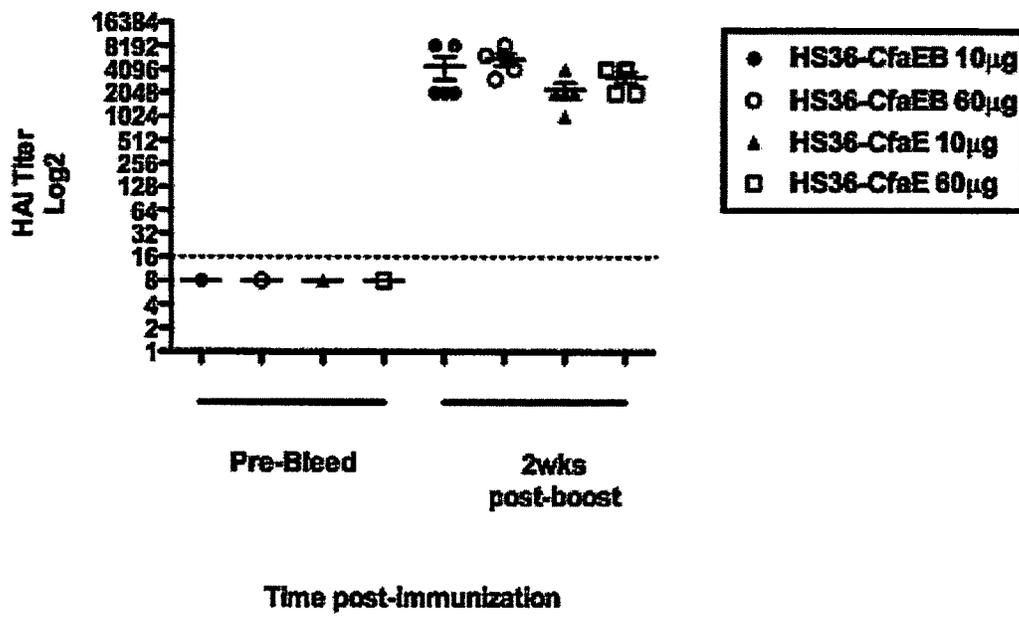


FIG. 5

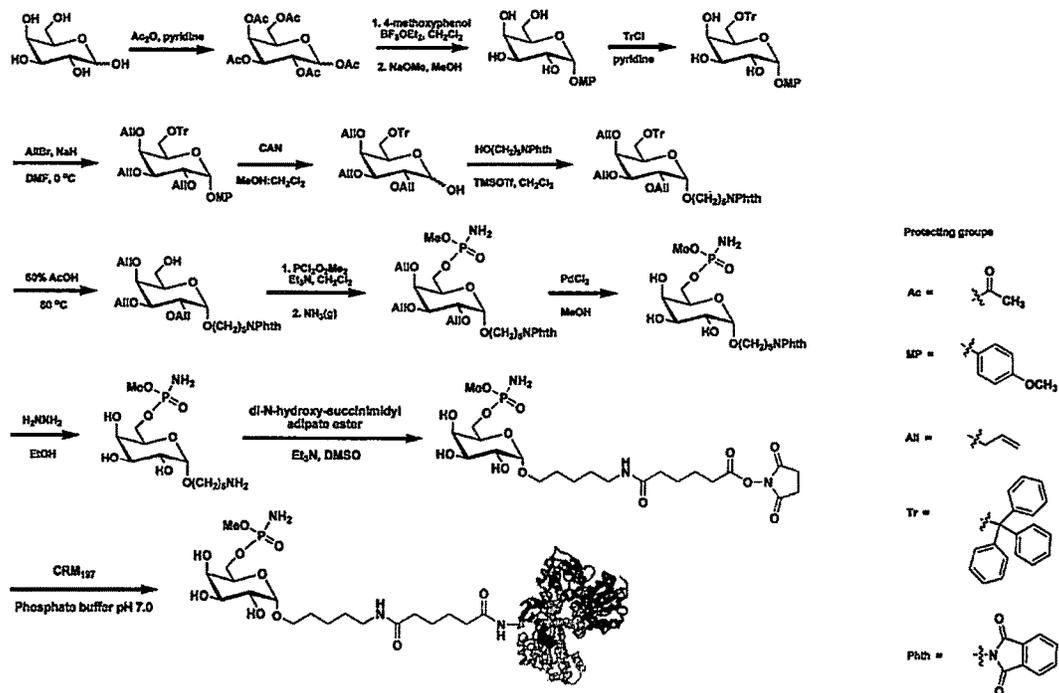


FIG. 6

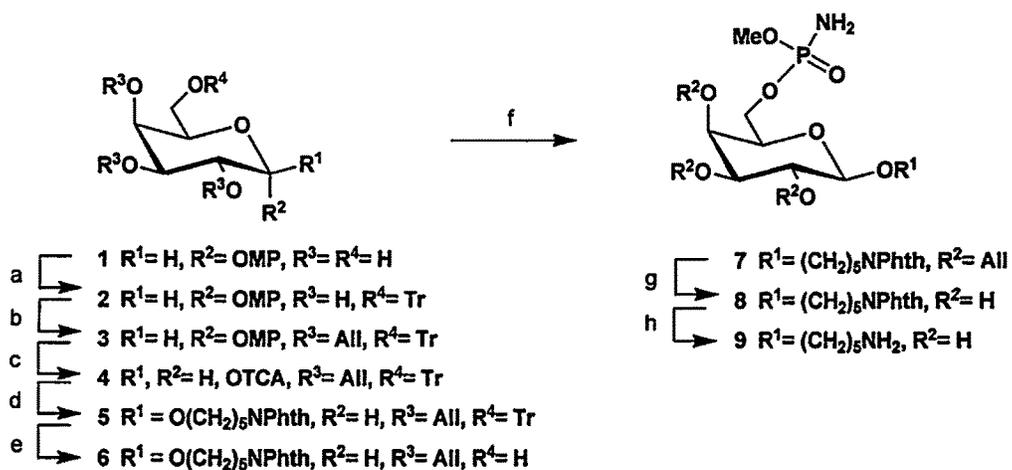


FIG. 7

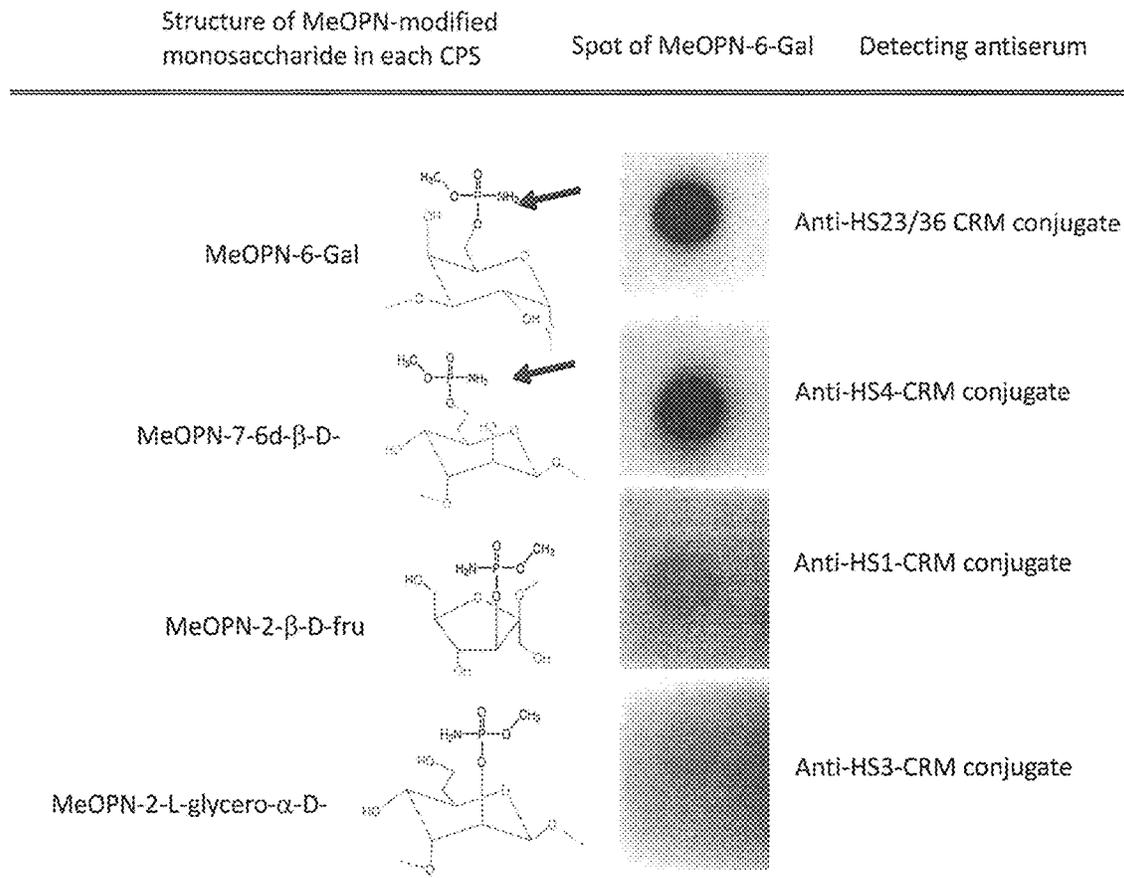
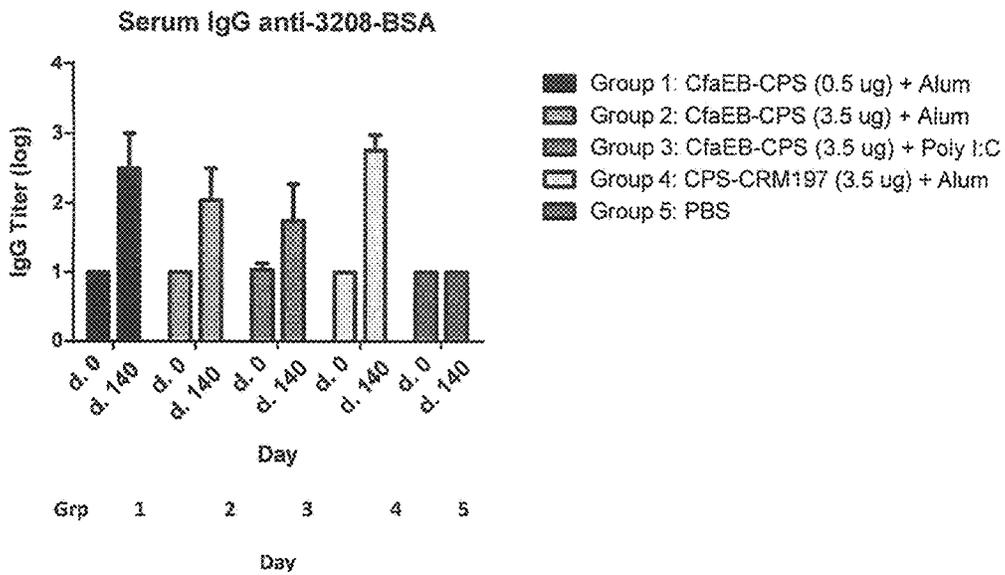


FIG. 8

A.



B.

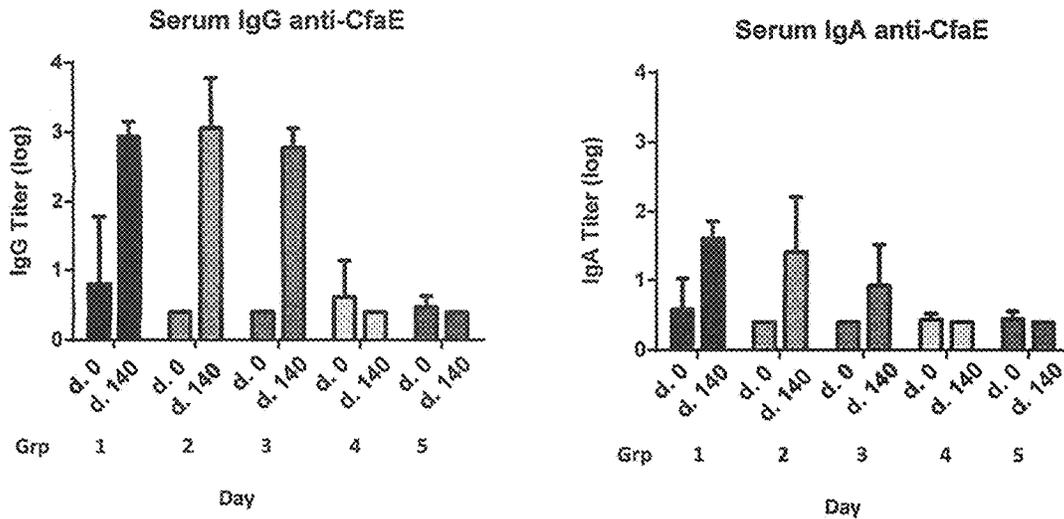


FIG. 9

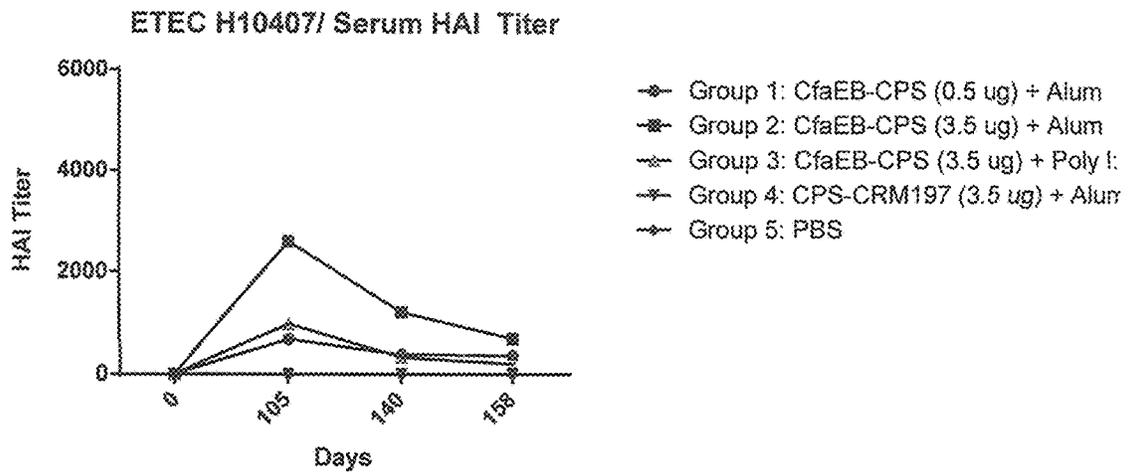


FIG. 10

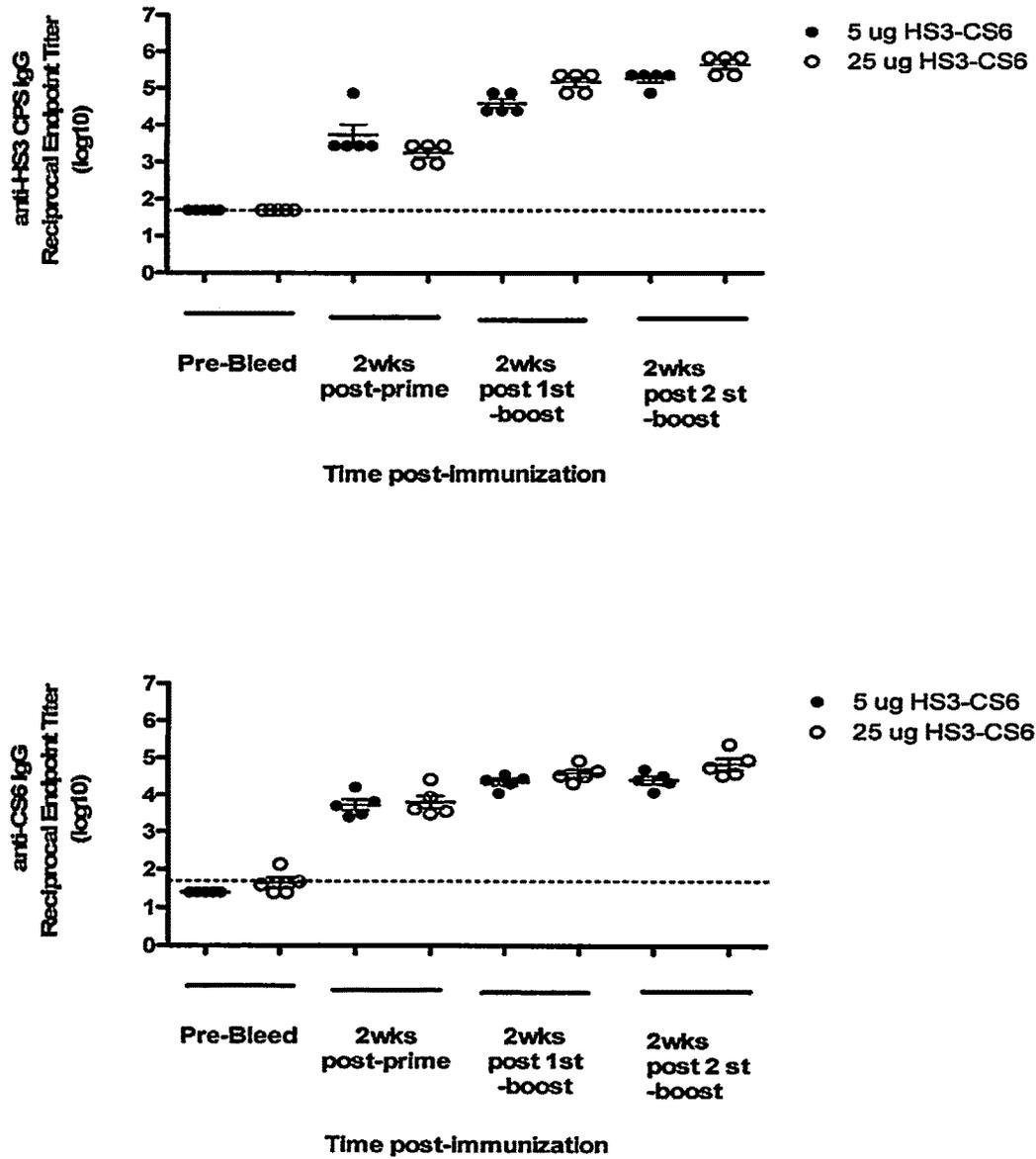


FIG. 11

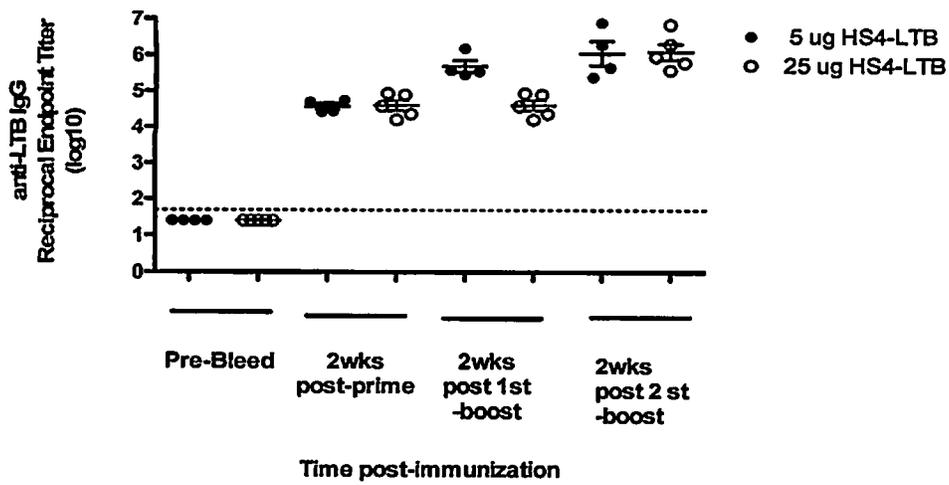
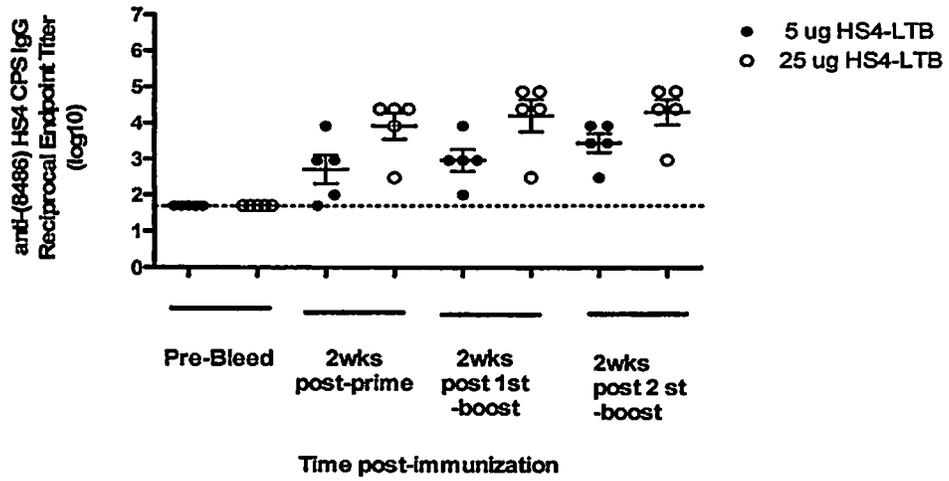


FIG. 12

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**COMBINED ENTEROPATHOGEN  
RECOMBINANT CONSTRUCT****CROSS-REFERENCES TO RELATED  
APPLICATIONS**

This application is a Continuation-in-Part to U.S. Non-provisional application Ser. No. 11/340,003, filed Jan. 10, 2006, which claims priority to U.S. Provisional application 60/642,771 filed Jan. 11, 2005, and a Continuation-in-Part to U.S. Nonprovisional application Ser. No. 11/524,057 filed Sep. 20, 2006, which claims priority to U.S. Provisional application 60/722,086, filed Sep. 21, 2005, and a Continuation-in-Part to U.S. Nonprovisional application Ser. No. 14/048,264, filed Oct. 8, 2013, which claims priority to U.S. Provisional application 61/727,943, filed Nov. 19, 2012, the contents of which are herein incorporated by reference. This application also claims priority to U.S. Provisional application 62/054,454, filed 24 Sep. 2014, U.S. Provisional application 62/127,927, filed Mar. 4, 2015, U.S. Provisional application 62/165,301, filed May 22, 2015, U.S. Provisional application 62/127,935, filed Mar. 4, 2015, and U.S. Provisional application 62/075,399, filed Nov. 5, 2014, the contents of which are herein incorporated by reference.

**BACKGROUND OF INVENTION****Field of the Invention**

The inventive subject matter relates to a recombinant construct against enterotoxigenic *Escherichia coli* and *Campylobacter jejuni* comprising a combined anti-ETEC recombinant polypeptide construct and *C. jejuni* capsular polysaccharide.

**Description of Related Art**

Enterotoxigenic *Escherichia coli* (ETEC), *Shigella*, spp. and *Campylobacter jejuni* (CJ) are major causes of bacterial diarrhea worldwide. Both pathogens are a serious health threat to western travelers and young children in resource-limited countries, making them apt target populations for a single or dual pathogen vaccine against ETEC and CJ. No FDA-licensed vaccines are available for either pathogen.

ETEC causes an estimated 210 million cases of diarrhea and 380,000 deaths annually among infants and young children. Moreover, ETEC is the most common cause of travelers' diarrhea. ETEC causes diarrhea ranging in severity from mild illness to severe cholera-like purging. There are two major virulence factors, adhesive fimbriae, dubbed colonization factors (CFs), and enterotoxins. Surface-expressed CFs, consisting of complex protein heteropolymers, mediate adherence to the small intestinal epithelium to initiate colonization within this privileged host niche. ETEC produce one or both of two different enterotoxins, a heat-labile (LT) and a heat-stable enterotoxin (STI). LT and STI intoxicate epithelial cells, resulting in fluid and electrolyte secretion and clinical diarrhea. LT is highly immunogenic and a potent adjuvant, while STI is a small, poorly immunogenic peptide.

Prevalent CFs and a non-toxic form of the LT (or its congener cholera toxin (CT)) have been the focus for several strategies to develop an ETEC vaccine. Such antigens have been used individually or bundled as components of a whole-cell killed vaccine, live vaccines vectored by attenuated ETEC or other enterobacterial species (e.g., *Shigella* and *Vibrio cholerae* 01), and purified protein vaccines. None has yet been shown to confer sufficiently high and broad levels of protection. The weight of evidence from clinical trials indicates that anti-LT immunity confers short-term

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protection against LT-producing ETEC. There is also evidence to show that certain CFs function as protective antigens. There are, however, significant challenges for ETEC vaccine development. For one, about half of all ETEC express only STI, for which anti-LT immunity is not thought to be effective, thus necessitating anti-CF or anti-bacterial immunity. Also, the diversity of ETEC CFs poses issues for achievement of sufficiently broad coverage with inclusion of a realistic number of CFs.

**SUMMARY OF THE INVENTION**

The invention relates to an immunogenic construct comprising a polypeptide construct expressing enterotoxigenic *Escherichia coli* (ETEC) fimbrial subunits combined with a *Campylobacter jejuni* capsular polysaccharide or *Shigella* spp lipopolysaccharide (LPS).

In a preferred embodiment, one or more *Campylobacter jejuni* capsular polysaccharides are conjugated to one or more *Escherichia coli* enterotoxigenic recombinant polypeptide constructs. In another embodiment, *Shigella* LPS is conjugated to the ETEC polypeptide construct.

*Campylobacter jejuni* is associated with induction of Guillain-Barré Syndrome (GBS), a post-infectious polyneuropathy that can result in paralysis. The association is due to molecular mimicry between the sialic acid containing-outer core of the lipooligosaccharide (LOS) and human gangliosides (5, 6, 89, 91). Thus, antibodies generated against LOS cores result in an autoimmune response to human neural tissue. Use of capsular polysaccharide from *C. jejuni* can induce an immune response without the possible induction of Guillain-Barré Syndrome.

In a preferred embodiment, the composition comprises an ETEC recombinant polypeptide construct design wherein major or minor subunits, derived from the same ETEC fimbrial type, are connected, via polypeptide linkers, and stabilized by donor strand complementation. The C-terminal most ETEC major subunit is connected, via a linker, to a donor strand region from an ETEC major subunit, which can be either homologous or heterologous to the C-terminal major subunit. The immunogenic composition can comprise a whole or an immunogenic fragment, containing a donor  $\beta$  strand region, of the ETEC fimbrial major or minor subunits. In some construct examples, in order to avoid inadvertent association of subunits, especially in CS6 subunits to each other, major ETEC fimbrial subunits can contain an N-terminal deletion of 14 to 18 amino acids.

In another embodiment one or more of the above constructs are connected, via a polypeptide linker, to form a multipartite fusion construct, wherein the subunits derived from multiple fimbrial types are expressed. In this embodiment, the fimbrial subunits can be derived from any ETEC fimbrial type, including, but not limited to: ETEC class 5 fimbriae type, including class 5a, 5b or 5c; ETEC CS3; and ETEC CS6.

The embodied multipartite construct can contain a deletion of the N-terminal region of one or more fimbrial subunits to avoid undesirable associations with other monomers or multimers and to remove reduce amino acid sequence length between polypeptides to reduce the protease cleavage.

DNA encoding the ETEC recombinant polypeptide construct can be used to express a polypeptide for attachment to *C. jejuni* or *Shigella* LPS. As such, an object of the invention also includes a use of a construct for immunizing mammals, including humans, by a composition comprising antigens from multiple bacterial species, including ETEC, *C. jejuni*

and *Shigella* strains. The embodied use comprises one or more priming administrations of the combination construct. The priming dose can be subsequently followed by one or more boosting doses.

#### BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1. Illustration of inventive construct design wherein major or minor subunits, derived from the same ETEC fimbrial type are connected, via polypeptide linkers and stabilized by donor strand complementation. The construct can contain a deletion of the N-terminal region of the N-terminal subunit. This feature prevents undesirable association with other monomers or multimers. The C-terminal subunit is stabilized by a donor  $\beta$  strand, connected to the subunit via a polypeptide linker, wherein the donor  $\beta$  strand is either derived from a homologous subunit, which is defined as a subunit that is the same as the subunit the donor strand is stabilizing or from a heterologous subunit, defined as derived from a subunit that is different still from the same fimbrial type.

FIG. 2 illustrates a multipartite construct wherein multiple compositions, illustrated in FIG. 1, are connected via a polypeptide linker. The first subunit, is a major or minor (e.g. ETEC class 5 adhesin) ETEC fimbrial subunit. One or more major ETEC fimbrial subunits are then connected to the first subunit and to each other via a linker, wherein the subunits are stabilized by donor strand complementation. The C-terminal most ETEC major subunit is connected, via a linker, to a donor strand region from an ETEC major subunit, which can be either homologous or heterologous to the terminal major subunit. In some construct examples, in order to avoid inadvertent association of subunits, especially in CS6 subunits to each other, major ETEC fimbrial subunits can contain an N-terminal deletion of 14 to 18 amino acids.

FIG. 3. SDS-PAGE and immunoblots of conjugate vaccines. A. Analyses of CfaE-HS36 conjugate. Lane 1-3 are stained with Gel Code Blue. Lane 1, Precision Plus Protein standards (BioRad); lane 2, CfaE; lane 3, CfaE-HS36 conjugate. Lanes 4-5 are immunodetected with anti-CfaE antibodies. Lane 4, CfaE; lane 5, CfaE-HS36 conjugate. Lanes 6-7 are immunodetected with antibodies to whole cells of 81-176 (HS36). Lane 6, CfaE-HS36 conjugate; lane 7, proteinase K digested whole cells of 81-176. B. Analyses of CfaEB-HS36 conjugate. Lane 1-3 are stained with Gel Code Blue. Lane 1, Precision Plus Protein standards (BioRad); lane 2, CfaEB; lane 3, CfaEB-HS36 conjugate. Lanes 4-5 are immunodetected with anti-CfaE antibodies. Lane 4, CfaEB; lane 5, CfaEB-HS36 conjugate. Lanes 6-7 are immunodetected with antibodies to whole cells of 81-176 (HS36). Lane 6, CfaEB-HS36 conjugate; lane 7, proteinase K digested whole cells of 81-176. The molecular weights of the protein markers are shown on the left.

FIG. 4. *jejuni* anti-CPS (A) or ETEC anti-CfaE (B) induced by HS36 conjugated to CfaE or CfaEB in mice.

FIG. 5. Functional antibodies, evidenced by HAI titer, induced in mice immunized with HS36 conjugate vaccines.

FIG. 6. Summary of synthesis of polysaccharide construct and conjugation to CRM<sub>197</sub>.

FIG. 7. Synthesis of aminopentanyl OMe-phosphoramidate galactoside. Reagent and conditions: (a) TrCl, pyridine, 95%; (b) AlIBr, NaH, DMF, 0° C., 89%; (c) CAN, CH<sub>3</sub>CN, H<sub>2</sub>O, 0° C.; then CCl<sub>3</sub>CN, K<sub>2</sub>CO<sub>3</sub>, CH<sub>2</sub>Cl<sub>2</sub>, 57% over 2 steps; (d) HO(CH<sub>2</sub>)<sub>5</sub>NPhth, TMSOTf, CH<sub>2</sub>Cl<sub>2</sub>, 65%; (e) 80% AcOH, 80° C., 78%; (f) PCl<sub>2</sub>O<sub>2</sub>Me<sub>2</sub>, Et<sub>3</sub>N, CH<sub>2</sub>Cl<sub>2</sub>, then NH<sub>3</sub>(g), 27%; (g) PdCl<sub>2</sub>, MeOH, 75%, (h) H<sub>2</sub>NNH<sub>2</sub>, EtOH, 82%.

FIG. 8. Capsule cross-reactivity to 6-MeOPN-Gal with antibodies to multiple conjugate immunogenic compositions.

FIG. 9. Serology of *A. nancymae* immunized with CfaEB-HS23-36 construct. Day 0 verses day 140.

FIG. 10. HAI titers of *A. nancymae* against ETEC strain H10407 expressing Cfa 1.

FIG. 11. Immune response of mice against HS3 capsule (top panel) and against CS6 (bottom panel) following immunization with an CsaBA-HS3 conjugate vaccine. The vaccine was administered at two doses, either 5  $\mu$ g or 25  $\mu$ g by weight.

FIG. 12. Immune response of mice to HS4 capsule (top panel) and to LTB (bottom panel) following immunization with an LTB-HS4 conjugate vaccine. The vaccine was administered at two doses, 5  $\mu$ g or 25  $\mu$ g by weight.

#### DETAILED DESCRIPTION OF PREFERRED EMBODIMENTS

The term enterobacteria, as used herein, refers to enterotoxigenic *Escherichia coli* (ETEC), *Campylobacter jejuni* or *Shigella* spp., which include: *Shigella dysenteriae*, *Shigella flexneri*, *Shigella Boydii* or *Shigella sonnei*. As used herein, an enterobacteria polysaccharide polymer is a polysaccharide polymer derived from enterobacteria. The term “polysaccharide antigen” as used herein refers to a capsule polysaccharide derived from *Campylobacter jejuni* (*C. jejuni* or *Campylobacter jejuni* capsule) or a lipopolysaccharide derived from *Shigella* spp. As used herein, “polysaccharide” refers to two or more monosaccharide units composing a carbohydrate polymer molecule. A “polysaccharide polymer” refers to two or more polysaccharide molecules connected together.

The terms “polypeptide,” “peptide,” and “protein” as used herein can be interchangeably used, and refer to a polymer formed of two or more amino acid residues, wherein one or more amino acid residues are naturally occurring amino acids. The term “amino acid sequence” refers to the order of the amino acids within a polypeptide. As used, herein, “oligomer” are polypeptides sequences comprising relatively few amino acids.

The term “recombinant polypeptide,” “recombinant polypeptide construct,” or “recombinant protein,” as used herein, refers to polypeptides or proteins produced by recombinant DNA techniques, i.e., produced from cells transformed by an exogenous DNA construct encoding the desired polypeptide or the desired protein. The term “recombinant construct” refers to the DNA encoding the recombinant polypeptide, recombinant polypeptide construct or recombinant protein.

The term “donor strand” or “donor  $\beta$  strand” refers to the N-terminal region of an ETEC fimbrial subunit that associates with another ETEC fimbrial subunit in donor strand complementation.

The term “immunogenic composition” refers to a formulation containing proteins or polypeptides or polysaccharides or polysaccharide polymers that induce a humoral and/or cellular immune response. The term “immunogenic coverage” or “spectrum of coverage” refers to the induction of humoral and/or cellular immune response against specific strains of bacteria under the “coverage.” The term “immunogenic fragment” refers to a polypeptide containing one or more B- or T-cell epitopes and is of sufficient length to induce an immune response or to be recognized by T- or B-cells. The term “derivative” refers to a polypeptide or nucleic acid sequence with at least 80% identity with sequence of the identified gene. In this context, “identity”

refers to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues that are the same, when aligned for maximum correspondence. Where some sequences differ in conservative substitutions, i.e., substitution of residues with identical properties, the percent sequence identity may be adjusted upwards to correct for the conservative nature of the substitution. Percent similarity refers to proportion of identical and similar (conserved change) residues.

"Fimbriae" are defined as projections or filaments on ETEC bacteria and are composed of major subunits, as in the case of CS3 and CS6 fimbriae or major and minor subunits, as in the case of class 5a, 5b and 5c ETEC. "Fibrillae" are narrow projections from a bacteria. CS3 and CS6 fimbriae can also be termed fibrillae due to their narrow characteristic. The term "fimbrial subunit" refers to the proteins that comprise ETEC fimbriae and is used interchangeably with "pilin." "Pilin," therefore, can refer to a "major" or "minor" "fimbrial subunit" that comprise ETEC fimbriae. A "minor fimbrial subunit" refers to the adhesin protein at the tip of class 5 ETEC fimbriae and is expressed in stoichiometrically low amounts compared to "major" subunits. The "minor fimbrial subunits" include, but are not limited to, CfaE, CsfD, CsuD, CooD, CosD, CsdD, CsbD and CotD. "Major fimbrial subunits" refers to the ETEC fimbrial proteins represented in stoichiometrically larger amounts in ETEC fimbriae, compared to "minor fimbrial subunits." "Major fimbrial subunits" include the ETEC class 5 proteins: CfaB, CsfA, CsuA2, CsuA1, CooA, CosA, CsdA, CsbA, CotA; the ETEC CS3 proteins: CstH, CstG; and the ETEC CS6 proteins: CsaA, and CsaB.

The pathogenesis of *Campylobacter jejuni* remains poorly understood in comparison with ETEC and the organism shares few virulence factors with better-characterized pathogens. *C. jejuni* is unusual, however, among enteric pathogens in that it expresses a polysaccharide capsule (CPS) that is one of its few confirmed virulence factors.

Because of the importance of ETEC and *C. jejuni* as pathogenic agents, a combined ETEC-CJ composition was constructed in order to afford protection against both agents. In one embodiment, a recombinant polypeptide construct, comprising fimbrial subunits from Class 5 ETEC strains is fused to a capsule polysaccharide from the *C. jejuni* strain 18-176.

In a preferred embodiment, one or more recombinant polypeptide ETEC constructs, comprising the ETEC fimbrial adhesion, are conjugated to isolated *C. jejuni* capsule polysaccharide (CPS). One or more of a number of ETEC recombinant constructs can be conjugated to one or more of a number of *C. jejuni* capsule polysaccharide structures. In the inventive construct, the ETEC recombinant construct operates both as an immunogen against ETEC and as a protein carrier molecule, presenting the *C. jejuni* polysaccharide. Examples of ETEC recombinant polypeptides and *C. jejuni* capsule polysaccharides that can be incorporated into a combined structure are given in the following examples.

In a preferred embodiment, the ETEC polypeptide construct can not only serve as antigen against ETEC but also serve as a protein carrier for polysaccharide antigens, such as *C. jejuni* capsule polysaccharide.

#### Example 1: Conjugation of ETEC Polypeptides to *C. jejuni* Capsule Polysaccharide (CPS)

In a preferred embodiment, ETEC recombinant polypeptides or polypeptide constructs are conjugated to *C. jejuni*

CPS. The CPS can be derived from a number of *C. jejuni* strains. In the embodiment, any CPS of any *C. jejuni* strain is envisioned to be conjugated to ETEC recombinant polypeptide constructs. Alternatively, *Shigella* LPS can be conjugated to ETEC recombinant polypeptide constructs.

The overall method of conjugating includes oxidizing *C. jejuni* CPS, for example, with NaIO<sub>4</sub> in sodium acetate (pH 4.0). Oxidized CPSs were desalted with a 5 kDa cutoff membrane by stirred ultrafiltration, which is subsequently lyophilized. ETEC proteins are then added. The stoichiometry protein to CPS can vary, however, a typical ratio is 1:2 protein to CPS by mass. The concentration of components can be by any method. However, for example, polysaccharide concentration was determined by anthrone assay and protein concentration was determined. NaCNBH<sub>3</sub> is then added. The conjugates are subsequently desalted by ultrafiltration and lyophilized. CPS (or *Shigella* LPS), ETEC proteins and conjugates were analyzed, for example by SEC-HPLC. Conjugates were also analyzed by SDS polyacrylamide gel electrophoresis (PAGE) and Gel Code® Blue (Pierce, Biotechnology, Inc, Lombard, Ill.) staining. Conjugates were detected by antibody-based assay using anti-CPS and anti-ETEC protein.

As an example of ETEC recombinant polypeptide and *C. jejuni* conjugation, the CPS from the *C. jejuni* strain 81-176 was conjugated to ETEC recombinant polypeptide construct CfaE (class 5 ETEC adhesin) or to the recombinant polypeptide construct CfaE linked, via a polypeptide linker, to the major subunit CfaB.

CPS *C. jejuni* capsule was purified from *Campylobacter jejuni* strain 81-176 (PG3208). This mutant, in which the galT gene was insertionally inactivated by chloramphenicol cassette, lacks all ganglioside mimicry in its lipooligosaccharide (LOS) core.

The cells were grown in porcine Brain-Heart Infusion (BHI) broth and sonicated to inactivate the cells. The CPS was extracted by hot water/phenol method previously employed for the same organism (Chen, et al., Carbohydr. Res. 243: 1034 (2008)). Cells were immersed in a water/phenol mixture (3:2 ratio by volume), which was heated to 67° C. with stirring for 4 hours. The suspension was cooled and separation of the mixture into two separate layers (the aqueous layer and the phenol layer) and extraction of the aqueous layer was performed. The aqueous layer was removed and the phenol/water extraction was repeated on residue, to maximize the yield. Aqueous layers from two extractions were pooled and boiled for 1.5 hours with the addition of acetic acid to a pH of 3.5. The aqueous layer was dialyzed against running water for 2 days and concentrated using a Millipore concentrator cell with a 5 kDa cutoff membrane. Trace amounts of residual RNA were removed by digestion with benzonase enzyme at 90 u/ml in 50 mM Tris-CCl/1 mM MgCl<sub>2</sub>, pH 8 overnight at 37° C. Benzonase was removed from CPS, then desalted and concentrated using stirred ultrafiltration with 30 and 5 kDa MWCO disc membranes, respectively.

The isolated CPS was oxidized with adding 40 mg of CPS to 40 mM NaIO<sub>4</sub> in sodium acetate pH 4 in the dark at 4° C. for 2 days. Oxidized CPS was desalted with 5 kDa cutoff membrane by stirred ultrafiltration and was subsequently lyophilized.

Prior to conjugation the ETEC proteins, for example dscCfaE and dscCfaEB, were transferred to 0.1M borate buffer at pH 9.0. Oxidized CPS was added to each ETEC protein at a ratio of 1:2, protein to CPS by mass, and then NaCNBH<sub>3</sub> was added at 2 times mass equivalent to CPS. The reaction was incubated 1 day at room temperature and

6 days at 37° C. in the dark with continuous stirring. The conjugates were desalted by stirred ultrafiltration with 30 kDa membrane and lyophilized. Conjugates of the CPS to dscCfaE and dscCfaEB was conducted by SEC-HPLC. and polyacrylamide gel (PAGE) (12.5%) electrophoresis.

In PAGE analysis, immunodetected with rabbit polyclonal antibodies to whole cells of 81-176 was used to detect CPS and to CfaE. The results of this study are shown in FIG. 3. Immunoblotting of both conjugates with anti-CfaE antisera confirmed that the proteins ran as high molecular weight conjugates with conjugates with apparent masses ranging from just higher than the mass of each respective protein to >250 kDa. Immunoblotting with antisera to formalin fixed whole cells of *C. jejuni* 81-176 confirms that capsular polysaccharide was conjugated to the proteins. As illustrated in FIG. 3, no unconjugated protein remained in either conjugation.

The results of FIG. 3 were confirmed in SEC-HPLC. In the SEC-HPLC, unoxidized and oxidized CPSs, ETEC proteins and conjugates were analyzed using SEC-HPLC with a TSKgel-G2000SW<sub>xt</sub> column (30 cm×7.8 mm ID) and TSKgel SW guard column run on an ICS-5000 Dionex system with 0.1 M phosphate at pH 6.8, 0.1 M sodium sulfate and 5% acetonitrile at 0.6 ml/min flow rate. Samples were monitored at 214 nm with Ultimate 3000 variable wavelength detector and RI detector, both from Dionex.

The results of the SEC-HPLC are shown in FIG. 4 for dscCfaEB and in FIG. 5 for dscCfaE. Analysis by matrix-assisted laser desorption/ionization (MALDI) is shown in FIG. 6, for dscCfaEB and FIG. 7 for CfaE.

Detection of the conjugates by refractive index (RI) on SEC-HPLC revealed that 45% and 50% of the polysaccharide remained unconjugated with the CfaE and CfaEB conjugates respectively. This is summarized in Table 1, which also illustrates that the conjugated molar ratio of CPS to CfaE was 4.8:1 and that of CPS to CfaEB was 4.4:1.

TABLE 1

	CfaE conjugate		CfaEB conjugate	
	CPS	CfaE	CPS	CfaEB
Final product (includes unconjugated CPS) % yield	49%		63%	
Sugar:protein mass ratio in final product	2	1	1.85	1
% unconjugated with respect to final product by SEC-HPLC RI detection	45%		50%	
Conjugated mass ratio	1	1.5	1	2.3
Molecular weight	5.5 kDa	41 kDa	5.5 kDa	57 kDa
Conjugated molar ratio	4.8	1	4.4	1

#### Example 2: Anti-Class 5 ETEC, CS3 or CS6 Constructs

Anti-ETEC constructs that are contemplated to be conjugated to *C. jejuni* polysaccharide comprise the structures as illustrated in FIG. 1 and FIG. 2. FIG. 1 illustrates the basic recombinant construct design. As diagrammed in FIG. 1 the construct design comprises one, or more ETEC major or minor fimbrial subunits or fragments of major fimbrial subunits, containing the donor strand, derived from the same ETEC fimbrial type, which are connected, via polypeptide linkers and stabilized by donor strand complementation. The construct can contain a deletion of the N-terminal region of the N-terminal subunit. This feature prevents undesirable

associations with other monomers or multimers. The C-terminal subunit is connected to and stabilized by a donor  $\beta$  strand, connected to the subunit via a polypeptide linker, wherein the donor  $\beta$  strand is either derived from the adjacent subunit (i.e., homologous) or from a different subunit of the same fimbrial type (i.e., heterologous).

FIG. 2 illustrates the basic multipartite construct, wherein multiple constructs as in FIG. 1, are connected forming a recombinant construct comprising two or more fimbrial types. As illustrated in FIG. 1, major or minor subunits from the same fimbrial type are connected via a polypeptide linker sequence. In the multipartite construct, two or more constructs, as in FIG. 1, are connected, via a linker polypeptide.

In the multipartite construct design, as in the basic design (compare FIG. 1 with FIG. 2), the first subunit (N-terminal) is a major or minor ETEC fimbrial subunit. Each additional subunit is connected to adjacent subunits via a polypeptide linker that enables rotary freedom of the molecular components. The subunits are associated with and stabilized via a donor strand complementation from a C-terminally adjacent subunit via a donor  $\beta$  strand, connected via a linker polypeptide, to the C-terminus of the stabilized subunit. In some embodiments, subunits can contain a deletion of 14 to 18 amino acids from its N-terminal end. Additionally, specific constructs can be constructed with or without signal peptides of 18 to 22 amino acids and with or without histidine tags at the C-terminus.

In the multipartite construct, subunits from the same fimbrial type are directly connected. Groupings of subunits from the same fimbrial type are then connected to other groupings of subunits from other fimbrial types. Fimbrial types include, but are not limited to ETEC class 5a, 5b, 5c, CS3 and CS6. For example a single construct can include subunits derived from any two or more of class 5a, 5b, 5c, CS3 and CS6 fimbrial types.

Multiple linker sequences can be utilized in connecting the individual subunits. Examples of specific linkers include the tetrapeptide of SEQ ID No. 5. Another example is a tri-glycine linker (i.e., G-G-G). In the inventive construct, in cis donor strand complementation is used to stabilize adhesins and adhesin-pilin fusions for representative Class 5a, 5b, and 5c adhesins.

The contemplated composition is designed to enable as wide a range of coverage of ETEC strains as possible. As such, in one embodiment, the contemplated composition and use is aimed at inducing immunogenic response against class 5a, 5b, 5c ETEC, as well as ETEC strains expressing CS3 or CS6 fimbrial components.

In a preferred embodiment, recombinant polypeptide ETEC constructs are conjugated to *C. jejuni* capsule polysaccharide (CPS). One or more of a number of ETEC recombinant constructs can be conjugated to one or more of a number of *C. jejuni* capsule polysaccharide structures. Examples of Class 5 ETEC recombinant polypeptides are listed in Table 2. In Table 2, minor subunits are stabilized by connection, via a polypeptide linker, to associated major subunits. Alternatively, a 12-16 amino acid donor strand, derived from the associated major subunit is connected to the minor subunit via a polypeptide linker. These polypeptides can also be linked as per FIG. 1 and FIG. 2 to lead to the example constructs listed in Table 3. These examples can then be conjugated to isolated *C. jejuni* capsule polysaccharide, as in Example 1.

TABLE 2

Immune coverage (fimbrial types)	Subunit	SEQ ID No.	SEQ ID No.
		Full length sequences including spd <sup>1</sup> (DNA/polypeptide) <sup>2</sup>	Mature sequences (DNA/polypeptide) <sup>2</sup>
Class 5a	CfaE	56/57	115/58
	CfaB	59/60	116/61
	CsfD	64/65	117/88
	CsfA	62/63	118/89
	CsuD	70/71	119/90
	CsuA2	68/69	120/91
	CsuA1	66/67	121/92
Class 5b	CooD	74/75	122/93
	CooA	72/73	123/94
	CsdD	78/79	124/95
	CsdA	76/77	125/96
	CosD	82/83	133/97
	CosA	80/81	126/98
	CsbD	44/45	127/46
	CsbA	47/48	128/49
Class 5c	CotD	50/51	129/52
	CotA	53/54	130/55
CS3	CstH	84/85	131/99
	CstG	86/87	132/101
CS6	CssA	134/135	1/2
	CssB	136/137	3/4

<sup>1</sup>“spd” refers to signal peptide. The mature polypeptide sequence, therefore, would be the full length minus the signal peptide.

<sup>2</sup>DNA sequence encodes mature protein.

TABLE 3

Fimbriae class represented	Construct (adhesin-pilin) example <sup>1</sup>	SEQ ID No. DNA/Protein <sup>3</sup>
Class 5a	dsc <sub>14CsfA</sub> CfaE-CfaB-CsuA2-CsfA	103/104
Class 5b	dsc <sub>14CsbA</sub> CsbD-CsbA-ntd <sub>15</sub> dsc <sub>14CooA</sub> CooA <sup>2</sup>	105/106
Class 5b	dsc <sub>15CooA</sub> CsbD-CsbA-CooA <sup>2</sup>	107/108
Class 5c	dsc <sub>14CotA</sub> CotD-CotA	109/110

<sup>1</sup>dsc refers to donor strand complementation. The number and subunit refers to the N-terminal amino acids of length represented by the number from the subunit indicated that is connected at the C-terminus of the construct and is serving to stabilize the C-terminal construct. For example, “dsc<sub>14CsfA</sub>” refers to the N-terminal 14 amino acids of CsfA connect to the C-terminus of the construct.

<sup>2</sup>Linkers polypeptides are GGG rather than DNKQ.

<sup>3</sup>Sequence in example contains a Leu-Glu-His<sub>6</sub> at the C-terminus.

An important feature of the anti-ETEC construct is the enhanced immune recognition of the fimbrial adhesion. The minor subunits (i.e., ETEC adhesin) of ETEC Class 5 fimbriae are stoichiometrically represented in very low numbers relative to the major subunit. Therefore, an important feature of the recombinant constructs is the vastly improved stoichiometric representation of the minor subunit in order to enhance immune recognition of the minor subunit. Additionally, since fimbrial subunits, such as CfaE, are relatively susceptible to proteolytic degradation outside of the fimbrial structure, stabilization of the adhesin is also important. Therefore, constructs are designed to express ETEC subunits stabilized from misfolding and degradation by donor strand complementation.

The donor  $\beta$  strand is provided by the major fimbrial subunit. For example, in the case of CfaE, stabilization is provided by the N-terminal region of CfaB. Engineering of dscCfaE by incorporation of a donor peptide strand from the N-terminus of the CFA/I major subunit CfaB at its C-terminus transformed an insoluble, unwieldy native, recombinant protein into a stable immunogenic composition (Savarino, U.S. Patent application publication no. 20060153878 (13 Jul. 2006)), which is incorporated by reference, herein.

Based on its atomic structure, dscCfaE is folded into a native,  $\beta$ -sandwich conformation, consisting of two half-

barrels, comprising the N-terminal adhesin domain (CfaEad) a short  $\alpha$ -helical connector, and the C-terminal pilin domain (CfaEpd). The molecule is functional in that it directly mediates MRHA of bovine and human erythrocytes, and generates neutralizing antibodies that act to inhibit MRHA and decorate the tips of CFA/I fimbriae on immunoelectron microscopy.

A fusion protein was engineered by genetic insertion of the coding sequence for mature major structural subunit of ETEC adhesin, such as CfaB, to the 3'-end of the minor subunit, such as CfaE. This concept was disclosed in Savarino, U.S. patent application (Ser. No. 11/340,003, filed Jan. 10, 2006), which is incorporated, herein. This molecule contains all three domains of the CFA/I fimbriae (i.e., ad, pd, and major subunit) in a ratio of 1:1:1, rather than that found in native fimbriae (ca. 1:1:1000).

A number of observations indicate the suitability of dscCfaE (cloned from ETEC strain E7473) as a vaccine antigen. First, sequencing of 31 different wild type alleles of cfaE from ETEC isolates of varying geographic origin and serotypes, show that the gene and predicted polypeptide sequence are nearly invariant, with three different nonsynonymous nucleotide changes at one site each in only five of these 31 alleles (Chattopadhyay, et al., J. Biol. Chem., 287(9): 6150-6158 (2012)). Hence, the target protein shows uniformity in natural ETEC bacterial populations.

Additionally, CfaE, a Class 5a fimbrial adhesin, is 80-81% identical with the other Class 5a minor subunits proteins adhesins CsuD of CS14 fimbriae and CsfD of CS4 fimbriae. CsuD and CsfD share 94% identity. This is considerably higher than the average identity with other Class 5b and 5c fimbrial adhesins (mean 50% identity).

Moreover, rabbit anti-dscCfaE serum cross-neutralizes CS4- and CS14-ETEC in the hemagglutination assay (HAI). A number of vaccination studies have been performed in small (rabbit and mice) and large (monkeys and cows) animals with various routes of administration and adjuvant combinations showing that dscCfaE is a potent immunogen that can elicit systemic and mucosal antibodies which recognize dscCfaE and CFA/I and are neutralizing (as measured by HAI assay).

An embodiment includes anti-class 5 ETEC constructs based on the construct design illustrated in FIG. 1, whereby the N-terminal subunit is an ETEC class 5 minor (i.e., adhesin) subunit, listed in Table 2, including CfaE, CsfD, CsuD, CooD, CsdD, CosD, CsbD and CotD, connected, via a polypeptide linker, to one or more ETEC major subunits, from the same ETEC class 5 type, listed in Table 2. The polypeptide linker can be any of a number of polypeptide sizes. In a preferred embodiment, the linker is a tetrapeptide with the polypeptide sequence of SEQ ID No. 5. The C-terminal class 5 subunit is connected to a donor  $\beta$  strand, derived from a homologous subunit and is typically 12-19 amino acids. In alternative embodiments, one or more major subunit can include a deletion of 12 to 16 amino acids from the N-terminal region of the subunit.

The design in FIG. 1, utilizes the concepts disclosed in Savarino, U.S. patent application (Ser. No. 11/340,003, filed Jan. 10, 2006)), including donor strand complementation to provide stabilized class 5 ETEC adhesin. Due to the homology of ETEC class 5 minor subunits and major subunits, FIG. 1 further contemplates multiple constructs incorporating the fimbrial subunits of Table 2, or derivatives of these polypeptides or DNA sequences.

The construct design, illustrated in FIG. 1, incorporates the donor strand complementation stabilization features of Savarino (U.S. patent application (Ser. No. 11/340,003, filed

Jan. 10, 2006)), and furthers it by incorporating multiple major subunits, from a specific ETEC type, into a single adhesin-pilin construct. For example, multiple class 5b major subunits can be connected to a class 5b adhesin (i.e., minor subunit). Embodiments include adhesin-pilin constructs containing Csb D (ETEC Class 5b fimbrial adhesin) and Cot D (ETEC Class 5c fimbrial adhesin). Examples, for illustration, of embodiments of adhesin-pilin ETEC class 5 adhesin-pilin constructs, representing Class 5a, 5b and 5c are shown in Table 3.

CS6 and CS3

Rabbit model (RITARD) studies suggest the colonization factor CS6 and CS3 has immune-protective potential (Svennerholm, et al., *Infect. Immun.* 56: 523-528 (1988); Svennerholm, et al., *Infect. Immun.* 58: 341-346 (1990)). As such, an important technical goal is to reproduce a stabilized CS6 expressing recombinant structure expressing CS6 antigens that maximally elicits antibody responses inhibitory to CS6-directed adhesion.

Unlike class 5 ETEC fimbriae, the fimbrial structures may function as polyadhesins rather than monadhesins (Zavialov, et al., *FEMS Microbiol. Rev.* 31: 478-514 (2007)). Extrapolation from related fimbriae, assembly of ETEC CS6 and CS3 may be mediated by donor strand complementation mediated process through association of a CS6 or CS3 subunit with the N-terminal donor strand region of an adjacent subunit. Additionally, protection against misfolding and proteolytic degradation may also be afforded through donor strand complementation.

Association of monomers of CS3 and CS6 was evaluated by visualization of the subunit proteins under denaturing and non-denaturing conditions in polyacrylamide gel electrophoresis (PAGE). For both CS3 and CS6 monomers, under denaturing conditions the proteins migrating at the expected sizes. Under non-denaturing conditions multiple size (i.e., ladders) are seen formed by multimeric association of the subunits.

CS6 Fimbriae

CS6 fimbriae comprise CssA and CssB. Whereas the two CS3 major subunits show little to no variation in polypeptide sequences, modest variation in CS6 proteins is observed. For example, greater than 90% identity is found in CS6 protein CssA and greater than 95% identity is found in CssB allotypes. Both CS6 structural proteins exhibit a relatively low level of variation (i.e., greater than 90% amino acid conservation), with greater variation in CssA and the mutations randomly distributed along the CssA polypeptide.

In order to design an effective immunogenic composition that would be suitable for inclusion in a vaccine formulation a number of criteria were devised for determination of suitable constructs. These included the ability to maintain a structure without unwanted self-association or assembly; thermostability; and ability to generate anti-CS6 IgG and IgA antibody levels similar to those elicited by immunization with CS6.

Monomeric CS6 subunit assembly appears to be mediated by donor strands from adjacent CS6 subunits, as discussed above. It is hypothesized that interaction to form these stable structures is mediated by inter-subunit interaction through donor strand complementation. Donor strand complementation also affords protection against misfolding and proteolytic degradation. Therefore, in a preferred embodiment,

multimeric CS6 constructs were developed to take advantage of these attributes of donor strand complementation. Additionally, multimeric expression provides more efficient manufacture over production of monomers.

In one embodiment, a construct conjugated to *C. jejuni* comprises a multimeric CS6 with one or more of the CS6 subunits, CssA and CssB, or allelic variation or derivatives, with the construct design configuration illustrated in FIG. 1. In a preferred embodiment, the construct comprises a dimer of CssB and CssA with CssB N-terminal to CssA (i.e., CssB-CssA).

As illustrated in FIG. 1, or FIG. 2, CS6 subunit association is stabilized by in cis donor  $\beta$  strand complementation. Donor strand complementation is afforded by linking a CS6 subunit at its C-terminus, to the donor  $\beta$  strand region of another CS6 subunit, via a tetrapeptide linker. The linker can be any of a number of polypeptide regions. However, in a preferred embodiment, the linker is either as in SEQ ID No. 5 or a triglycine linker. In the case of a terminal CS6 subunit, stabilization is provided by donor  $\beta$  strand, connected at its C-terminus, from a homologous or heterologous CS6 subunit. Homologous subunit is defined as two subunits of the same form (e.g., CssA OR CssB). Heterologous subunits are of different forms (e.g., one is derived from CssA the other from CssB). The CS6 donor  $\beta$  strand is typically the N-terminal 14-16 amino acid region of CS6 subunit. The recombinant protein can be constructed with or without hexahistidine affinity tags, which are typically on the C-terminus.

Additionally, to prevent recombinant polypeptide constructs forming molecular associations resulting in undesirable non-covalent oligomer formation, in a preferred embodiment, the N-terminal 14-16 amino acids of the N-terminal CS6 subunit is deleted. As an illustration, "dsc<sub>B14</sub>CssBA" would contain a heterologous donor strand (i.e., "dsc"), from CS6 CssB, inserted at the C-terminus of the construct. In this case, the donor strand is 14 amino acids in length, as indicated by the "14." Similarly, a constructed designated "ntd<sub>15</sub>dsc<sub>4</sub>CssBA" would contain a homologous donor strand at the C-terminus of the construct and also comprises a deletion of the N-terminal amino acid region (termed "ntd").

Examples of constructs comprise one or more CS6 subunits with amino acid sequences selected from the group consisting of SEQ ID No. 2 (CssA) or SEQ ID No. 4 (CssB), or derivatives of these polypeptides. The DNA sequence for CssA is SEQ ID No. 1 and for CssB, SEQ ID No. 3. The subunits are connected by a polypeptide linker sequences. In a preferred embodiment, the linker is a tetrapeptide with the amino acid sequence of SEQ ID No. 5.

CS3 Fimbriae

Savarino (U.S. patent application Ser. No. 11/340,003 (2006)) discloses donor strand complementation stabilized ETEC constructs. Embodiments of this application incorporate the donor strand stabilization of CstH and adds the second CS3 subunit, CstG. Embodiments herein add additional features found to be important for stabilization of the CS3 subunits and immunogenicity against CS3. CS3 comprises CstH and CstG. The CS3 structural protein CstH is invariant. CstG is also highly conserved, showing 99-100% identity in polypeptide sequence for 39 wildtype CS3 genes

sequenced. Similarly, although some variation CstG is observed, it is also relatively invariant, with 99-100% amino acid conservation.

CS3 contains both CstG and CstH, in near equal amounts. Therefore, dimeric constructs were devised incorporating CstG and CstH, according to the template construct design of FIG. 1.

In one embodiment a polypeptide construct conjugated to *C. jejuni* capsule polysaccharide comprises a CS3 construct designed according to FIG. 1. In FIG. 1, CS3 constructs comprise one or more CS3 fimbrial subunits connected via a polypeptide linker. The C-terminal fimbrial subunit is connected, via a polypeptide linker, to a donor  $\beta$  strand region of a CS3 fimbrial subunit. The C-terminal donor  $\beta$  strand can be derived from the same CS3 subunit to which it is connect (i.e., homologous) or derived from a different subunit (i.e., heterologous). The polypeptide linker can be any number of polypeptide regions, however, in a preferred embodiment, the linker is a tetrapeptide of the sequence of SEQ ID No. 5, or a triglycine (i.e., G-G-G). The donor  $\beta$  strand region is the N-terminal 14-16 amino acids of the mature CstH or CstG protein. In alternatives of this embodiment, the first 14-18 amino acids of the N-terminal region of the N-terminal most subunit is deleted to avoid undesirable associations.

In a preferred embodiment, the CS3 construct is a dimer. Although other examples are contemplated using the design of FIG. 1, as an illustrative example, the recombinant polypeptide construct can be configured as "dsc<sub>16CstH</sub>CstG-linker)-CstH". In this example, the mature CstG polypeptide (SEQ ID No. 101) or full length polypeptide sequence (SEQ ID No. 87) is connected at its C-terminus to CstH polypeptide (SEQ ID No. 99), via a polypeptide linker. In this example, the CstH polypeptide, is connected, at its C-terminus, to a donor  $\beta$  strand region of 16 amino acids derived from CstH via a polypeptide linker.

Other examples can include constructs, according to FIG. 1. In other examples, the C-terminal donor  $\beta$  strand can be either homologous (derived from the same subunit) or heterologous (derived from a different subunit) to the C-terminal most CS3 fimbrial subunit.

#### Construction of Multipartite Fusion Constructs

Immunity to multiple strains of ETEC is important to obtain the greatest extent of anti-ETEC immunity. Toward this goal, recombinant polypeptide constructs were developed comprising two or more subunits derived from different ETEC fimbrial types according to the design illustrated in FIG. 2 to form multipartite fusion constructs. As used, herein, multipartite fusion or multipartite fusion constructs are recombinant polypeptide constructs according to FIG. 2. In this design, different ETEC fimbrial types are defined as fimbrial proteins derived from fimbriae of different strain ETEC types, as listed in Table 4 or 5, or derivatives of these polypeptides or DNA sequences. For example, the fimbrial type "CS3" comprises CstH and CstG. The fimbrial type "CS6" comprises CsaA and CsaB. The fimbrial types of Class 5 ETEC include the fimbrial types Class 5a, Class 5b and Class 5c.

In a preferred embodiment, major and/or minor subunits, derived from the same ETEC fimbrial type are connected, via polypeptide linkers, and stabilized by donor  $\beta$  strand complementation, as illustrated in FIG. 1. A multipartite fusion comprises one or more fimbrial subunits of the same

fimbrial type, as in FIG. 1, connected to one or more fimbrial subunits derived from a different fimbrial type as illustrated in FIG. 2.

In one embodiment, the multipartite fusion construct can include a deletion of the N-terminal region of one or more fimbrial subunits, but is preferably on the N-terminal most fimbrial subunit for a given ETEC fimbrial type, as illustrated in FIG. 2. This feature prevents undesirable associations with other monomers or multimers. The size of the deletion of the N-terminal region is 14 to 18 amino acids. In other embodiments, multipartite fusion constructs comprising Class 5 adhesins do not contain a deletion of the N-terminal region.

As illustrated in FIG. 2, the C-terminal subunit, for an ETEC fimbrial type, is connected to and stabilized by a donor  $\beta$  strand, connected to the subunit via a polypeptide linker, wherein the donor  $\beta$  strand is either that derived from the adjacent subunit (i.e., homologous) or from a different subunit of the same fimbrial type (i.e., heterologous). The size of the N-terminal donor strand depends on the fimbrial type and subunit stabilized. In preferred embodiments, for class 5 fimbrial subunits, the donor  $\beta$  strand, derived from the N-terminal region of the class 5 subunit stabilized, is 12 to 16 amino acids. For CS3 and CS6 subunits, the donor  $\beta$  strand is 14 to 16 amino acids. As mentioned above, the construct can contain a deletion of the N-terminal region of the N-terminal subunit. This feature prevents undesirable associations with other monomers or multimers. The size of the deletion of the N-terminal region is 14 to 18 amino acids.

As illustrated in FIG. 2 multiple constructs as in FIG. 1 are connected forming a recombinant polypeptide construct comprising two or more ETEC fimbrial types. In this way, one or more major or minor subunits, derived from the same ETEC fimbrial type, are connected via polypeptide linkers and stabilized by donor strand complementation. In another embodiment, one or more glycine residues separates different ETEC fimbrial types, acting as a "swivel" means between the ETEC types. The glycine residue, due to its small, unbranched molecular characteristics, enables rotary freedom of the molecular components. Subunits derived from the same fimbrial type (as in FIG. 1) are connected by a polypeptide linker, with the subunits stabilized by donor strand complementation. As shown in FIG. 2, the C-terminal subunit of each ETEC fimbrial type is stabilized by a donor strand that is homologous or heterologous to the C-terminal subunit of that fimbrial type.

In other embodiments, the construct can contain an N-terminal deletion at the N-terminus of the entire construct as well as an additional deletion, of 14 to 18 amino acids, at the N-terminus of the first "internal" subunit that is of a different fimbrial type. This is illustrated in FIG. 2. In the case of the deletion on the N-terminus of the "internal" subunit, the deletion serves to shorten the length between subunits, thus reducing the likelihood of misfolding and proteolytic cleavage. In another embodiment, a donor  $\beta$  strand, derived from a homologous or heterologous subunit, is inserted at the C-terminus of the C-terminal CS6 or CS3 subunit. For class 5 fimbrial subunits, the donor  $\beta$  strand, derived from the N-terminal region of the class 5 subunit that is stabilized, is 12 to 16 amino acids. For example, in preferred embodiments, CfaB is stabilized by a 14 amino acid donor  $\beta$  strand; CsaA by a 14 amino acid donor  $\beta$  strand; CsaB by a 15 amino acid donor  $\beta$  strand, CooA by a 14 amino acid donor  $\beta$  strand and CotA by a 14 amino acid donor  $\beta$  strand. For CS3 and CS6 subunits, the donor  $\beta$  strand is 14 to 16 amino acids, with preferred embodiments of CS3 fimbrial subunits (i.e., CstH or CstG) stabilized by a 16 amino acid donor  $\beta$

strand derived from CstH or CstG; and CS6 fimbrial subunits (i.e., C<sub>55</sub>A or C<sub>55</sub>B) stabilized with a 16 amino acid donor  $\beta$  strand derived from C<sub>55</sub>A or C<sub>55</sub>B. However, other donor  $\beta$  strand lengths are envisioned.

The inventive compositions can utilize different linker sequences. In a preferred embodiment, the linker contains the amino acid sequence of SEQ ID No. 5. In another embodiment, the linker is a tri-glycine linker. In other embodiments, the C-terminal end of the construct contains a histidine tag for purification of the construct.

In the inventive construct, in cis donor strand complementation is used to stabilize adhesins and adhesin-pilin fusions for representative Class 5a, 5b, and 5c adhesins. For each adhesin target group, in a preferred embodiment, the compositions are constructed with the intent of eliciting anti-adhesive immune responses. Further towards this goal, Class 5 multipartite fusions comprising Class 5 adhesin minor subunits are typically constructed such that the adhesin (i.e., minor fimbrial subunit) is located at the N-terminus of the constructed with the minor fimbrial subunit linked at its C-terminus to one or more major subunits, followed at the terminal end of the construct with the donor  $\beta$ -strand of the last major subunit.

Other embodiments include constructs comprising Class 5a adhesin CfaE tandemly linked at its C-terminus to one or more of CfaB (CFA/I major subunit), CsuA2 (CS14 major subunit) and CsfA (CS4 major subunit); Class 5b adhesin CsbD tandemly linked at its C-terminus to one or more of CsbA (CS17 major subunit), which shares high identity to the CS19 pilin subunit CsdA, and CooA (CS1 major subunit), which shares high identity to the PCFO71 pilin subunit CosA; and Class 5c adhesin CotD tandemly linked at its C-terminus to CotA (CS2 major subunit).

Embodiments of ETEC multipartite fusion constructs are illustrated in Table 4 and 5. In this embodiment, constructs comprise any major or minor ETEC fimbrial subunit from Table 2 in multiple combinations, connected by linker polypeptides and stabilized from proteolytic degradation by donor strand complementation utilizing the design illustrated in FIG. 2. Table 2 lists the ETEC fimbrial subunits (major and minor subunits) than can be used and incorporated into the multipartite fusion construct design of FIG. 2, which can then be conjugated to *C. jejuni* capsule polysaccharide or *Shigella* LPS. Any subunit, therefore, is combined with one or more other ETEC major subunits from any ETEC fimbrial phenotypic type, including Class 5a, 5b, 5c, CS3 and CS6.

The recombinant polypeptide construct motif comprises a whole or immunogenic fragment of a minor or major ETEC fimbrial subunit connected at its C-terminal end to a linker. The linker is connected at its C-terminus to a whole major ETEC fimbrial subunit or a polypeptide donor strand of an ETEC major structural subunit, derived from the same fimbrial type. The whole ETEC major subunit or donor strand polypeptide is then connected, via a linker at its C-terminal end, to one or more additional major structural fimbrial subunits, derived from the same fimbrial type, from Table 2.

The strategy for selecting and developing specific genetic fusion constructs is guided, in part, by the phylogenetic and antigenic relatedness of subunits. For example, constructs containing Class 5a, 5b and 5c pilin subunits are selected based on the relatedness of minor and major subunits within a particular ETEC fimbrial class (i.e., class 5a, 5b or 5c). As such, adhesin (i.e., minor fimbrial subunit) from a specific fimbrial type (e.g., Class 5a) are linked to Class 5a major subunits. Further selection of subunits is guided and based on epidemiological study analysis in order to achieve opti-

mum immunogenic coverage of ETEC strains. What *C. jejuni* capsule polysaccharide to conjugate is predicated primarily on epidemiological data suggesting pathogenicity of the strain providing the capsule polysaccharide. Although many *C. jejuni* strains exist, most are not pathogenic.

In the multipartite constructs listed in Table 4 and 5 the linker polypeptide, depending on the example construct, can comprise a four (4) amino acid sequence (tetrapeptide) or a tri-glycine. Also, as illustrated in FIG. 2, the subunits are interconnected and stabilized by donor strand complementation, which is denoted by "dsc". In this nomenclature, the fimbrial subunit derivation is also indicated. For example, in the construct "dsc<sub>16C<sub>55</sub>H</sub>CstG-CstH-(G)-ntd<sub>5</sub>dsc<sub>16C<sub>55</sub>A</sub>C<sub>55</sub>A-C<sub>55</sub>B", the N-terminal CS3 subunit "CstG" is connected, via a linker, to the CS3 subunit "CstH", which is connected, via a linker, to a donor strand of 16 amino acids derived from "CstH." Similarly, the N-terminal CS6 subunit "C<sub>55</sub>B" is connected, via a linker, as illustrated in FIG. 2, to a 16 amino acid donor strand derived from "C<sub>55</sub>A." In this example, donor strand complementation of the "C<sub>55</sub>B" subunit is via a heterologous donor strand (i.e., derived from "C<sub>55</sub>A").

In Table 4 and 5 the examples contain a "G" (i.e., glycine) to provide a "swivel." Also, in some examples, the N-terminal region of N-terminal CS6 subunit is deleted (delineated by "ntd") to avoid undesirable association with other CS6 subunits, as described above. It should be noted that, in addition to the examples illustrated in Table 4 or 5 (or Table 3), other combinations of major and minor subunits are contemplated utilizing the construct design illustrated in FIG. 2 and the fimbrial subunits of Table 2. In some sequences listed, a six (6) histidine (i.e., His<sub>6</sub>) tag is inserted. The constructs can be designed to include the histidine (i.e., His<sub>6</sub>) tag or designed without this tag region. Additionally, some sequences contain the signal peptide (designated "spd" in Table 2 and 3) region. Constructs can be constructed with or without this region, as well, which may be added to improve manufacturing efficiency of the multipartite fusion construct.

TABLE 4

Fimbrial type (SEQ ID No. DNA/Protein)	Examples of CS3 containing constructs <sup>1,2,4,5</sup>
Class 5a/CS3 (6/7)	dsc <sub>14C<sub>55</sub>B</sub> -CfaE-CfaB-(G <sup>3</sup> )-ntd <sub>18</sub> dsc <sub>16C<sub>55</sub>H</sub> CstG-CstH
Class 5a/CS3 (8/9)	dsc <sub>14C<sub>55</sub>A</sub> CfaE-CfaB-CsuA2-CsfA-(G)-ntd <sub>18</sub> dsc <sub>16C<sub>55</sub>H</sub> CstG-CstH
Class 5b/CS3 (10/11)	dsc <sub>14C<sub>55</sub>B</sub> CsbD-CsbA-ntd <sub>15</sub> dsc <sub>14C<sub>55</sub>A</sub> CooA-(G)-ntd <sub>18</sub> dsc <sub>16C<sub>55</sub>H</sub> CstG-CstH
Class 5c/CS3 (12/13)	dsc <sub>14C<sub>55</sub>A</sub> CotD-CotA-(G)-ntd <sub>18</sub> dsc <sub>16C<sub>55</sub>H</sub> CstG-CstH
CS3/toxin fusion (36/37)	dsc <sub>16C<sub>55</sub>H</sub> CstG-CstH-sCTA2
LTB multimeric composition (38/39)	LTB <sub>5</sub>
CS3/CS6 (14/15)	dsc <sub>16C<sub>55</sub>H</sub> CstG-CstH-(G)-ntd <sub>15</sub> dsc <sub>16C<sub>55</sub>A</sub> C <sub>55</sub> A-C <sub>55</sub> B
CS6/CS3 (34/35)	ntd <sub>14</sub> dsc <sub>16C<sub>55</sub>B</sub> C <sub>55</sub> B-C <sub>55</sub> A-(G)-ntd <sub>18</sub> dsc <sub>16C<sub>55</sub>H</sub> CstG-CstH

<sup>1</sup>All combinations can include a histidine (i.e., His<sub>6</sub>) at the C-terminal end.

<sup>2</sup>Subunits can be linked via either DNKQ or tri-glycine linker.

<sup>3</sup>(G) refers to glycine residue introduced to provide a "swivel."

<sup>4</sup>"ntd" refers to N-terminal deletion (excised from mature protein) with extent of deletion (i.e., amino acids) indicated.

<sup>5</sup>"dsc" refers to span of N-terminal residues from donor  $\beta$ -strand, its amino acid length and its source.

TABLE 5

Fimbrial type (SEQ ID No. DNA/Protein)	Examples of CS6 containing constructs
CS6/CS3 (34/35)	ntd <sub>14</sub> dsc <sub>16C<sub>33B</sub></sub> CssB-CssA-(G)-ntd <sub>18</sub> dsc <sub>16C<sub>33H</sub></sub> CstG-CstH
CS3/CS6 (32/33)	dsc <sub>16</sub> CstG-CstH-(G)-ntd <sub>14</sub> dsc <sub>16C<sub>33B</sub></sub> CssB-CssA
Class 5b/CS6 (28/29)	spd <sub>19</sub> dsc <sub>14C<sub>33A</sub></sub> CotD-CotA-(G)-ntd <sub>14</sub> dsc <sub>16C<sub>33B</sub></sub> -CssB-CssA
Class 5b/CS6 (30/31)	dsc <sub>14C<sub>33A</sub></sub> CotD-CotA-(G)-ntd <sub>14</sub> dsc <sub>16C<sub>33B</sub></sub> -CssB-CssA
Class 5b/CS6 (24/25)	spd <sub>19</sub> dsc <sub>15C<sub>33A</sub></sub> CsbD-(GGG)-CsbA-(GGG)-ntd <sub>14</sub> dsc <sub>14C<sub>33A</sub></sub> CooA-(G)-(GGG)-ntd <sub>14</sub> dsc <sub>16C<sub>33B</sub></sub> CssB-CssA
Class 5b/CS6 (26/27)	dsc <sub>15C<sub>33A</sub></sub> CsbD-(GGG)-CsbA-(GGG)-ntd <sub>14</sub> dsc <sub>14C<sub>33A</sub></sub> CooA-(G)-(GGG)-ntd <sub>14</sub> dsc <sub>16C<sub>33B</sub></sub> CssB-CssA
Class 5a/CS6 (16/17)	dsc <sub>14C<sub>33A</sub></sub> CfaE-CfaB-(G)-ntd <sub>16</sub> dsc <sub>16C<sub>33A</sub></sub> CssB-CssA
Class 5a/CS6 (113/114)	dsc <sub>14C<sub>33A</sub></sub> CfaE-CfaB-(G)-ntd <sub>16</sub> dsc <sub>16C<sub>33B</sub></sub> CssB-CssA
Class 5a/CS6 (18/19)	dsc <sub>14C<sub>33A</sub></sub> CfaE-CfaB-(G)-ntd <sub>16</sub> dsc <sub>16C<sub>33B</sub></sub> CssA-CssB
Class 5a/CS6 (111/112)	dsc <sub>14C<sub>33A</sub></sub> CfaE-CfaB-(G)-ntd <sub>16</sub> dsc <sub>16C<sub>33A</sub></sub> CssA-CssB
CS3/CS6 (101/102)	dsc <sub>16C<sub>33A</sub></sub> CssA-CssB-(G)-ntd <sub>18</sub> dsc <sub>16C<sub>33H</sub></sub> CstG-CstH
Class 5a/CS6 (22/23)	dsc <sub>14C<sub>33A</sub></sub> CfaE-CfaB-CsuA2-CsfA-(G)-ntd <sub>14</sub> dsc <sub>16C<sub>33B</sub></sub> CssB-CssA
Class 5a/CS6 (20/21)	spd <sub>22</sub> dsc <sub>14C<sub>33A</sub></sub> CfaE-CfaB-CsuA2-CsfA-(G)-ntd <sub>14</sub> dsc <sub>16C<sub>33B</sub></sub> CssB-CssA
CS6-chimera (40/41)	ntd <sub>14</sub> dsc <sub>16C<sub>33B</sub></sub> CssB-CssA-sCTA2
CS6-chimera (42/43)	ntd <sub>15</sub> dsc <sub>16C<sub>33A</sub></sub> CssA-CssB-sCTA2

<sup>1</sup>All combinations can include a histidine (i.e., His<sub>6</sub>) at the C-terminal end.

<sup>2</sup>Subunits can be linked via either DNKQ or tri-glycine (GGG) linker. In preferred embodiments, DNKQ is used, except where indicated with (GGG).

<sup>3</sup>(G) refers to glycine residue introduced to provide a "swivel".

<sup>4</sup>"spd" refers signal peptide. Number indicates number of amino acids.

<sup>5</sup>"ntd" refers to N-terminal deletion (excised from mature protein) with extent of deletion (i.e., amino acids) indicated.

<sup>6</sup>"dsc" refers to span of N-terminal residues from donor β-strand, its amino acid length and its source.

In another embodiment, recombinant polypeptide constructs can contain a C-terminal toxin A subunit, such as cholera toxin A2 (CTA) to form a chimeric molecule. In this embodiment, a full-length or truncated CTA2 is connected to CS6 or CS3 multimeric recombinant polypeptide construct, such as a CS6 or CS3 dimer.

Examples of these toxin constructs are illustrated in Table 4 and 5. In these constructs, the LTB gene and the CS3 or CS6-toxin chimera are separately expressed. LTB, once expressed, would self assemble to form a pentameric structure. The ensuing LTB multimeric composition (i.e., LTB<sub>5</sub>) and CS3 or CS6-toxin chimera then non-covalently associate to form a holotoxin-like heterohexamer.

Although other examples are contemplated, the sequences of examples of illustrative chimeric constructs, containing a C-terminal toxin component, are illustrated in Table 4 (for CS3) and Table 5 (for CS6).

For CS3-chimeric molecules, one or more CS3 fimbrial subunits are connected, as in FIG. 1, via a polypeptide linker, preferably a tetrapeptide or triglycine. The C-terminal most CS3 fimbrial subunit is then connected to a donor β strand, via a polypeptide linker. The donor strand can be homologous or heterologous to the C-terminal fimbrial subunit. The donor strand is then connected to a toxin fragment, such as CTA2. The CS3-chimera example shown in Table 4, comprise the polypeptide sequence of SEQ ID

No. 37, which is encoded by the DNA sequence of SEQ ID No. 36. In this example, the N-terminal fimbrial subunit is CstG with a pelB leader (22 amino acids) connected at its N-terminal end (see FIG. 13). However, different ordering of CS3 fimbrial subunit units is contemplated. Also, in this example, the CstH is connected, via a polypeptide linker, to a 16 amino acid donor strand derived from the N-terminal 16 amino acids of CstH, which is connected to an A2 toxin fragment (i.e., CTA2). In a preferred embodiment, LTB is also expressed. LTB comprises the amino acid sequence of SEQ ID No. 39 and is encoded by the nucleotide sequence of SEQ ID No. 38. Once expressed, the LTB sequence would self assemble into a pentamer and associate, non-covalently, with the CS3-chimera to form a hetero-hexameric holotoxin-like structure.

CS6 toxin chimera examples are also illustrated in Table 5. For CS6 chimeras, as in CS3, one or more CS6 fimbrial subunits are connected via a polypeptide linker, preferably a tetrapeptide or triglycine. The C-terminal most CS6 fimbrial subunit is then connected to a donor β strand, via a polypeptide linker. The donor strand can be homologous or heterologous to the C-terminal fimbrial subunit. The donor strand is then connected to a toxin component (e.g., CTA2). In a preferred embodiment, like for CS3, the chimera is co-expressed, with LTB, which self assembles into a pentamer to form a non-covalent association with the chimeric adhesion-toxoid fusion molecule.

Although many additional combinations are possible, in the examples shown in Table 5, the constructs are dimers of CS6 subunits, connected via a tetrapeptide linker, with the C-terminal fimbrial subunit connected, via a tetrapeptide linker to a donor β strand. The donor β strand can be homologous or heterologous to the C-terminal most fimbrial subunit. However, in the examples in Table 5 the donor strands are heterologous to the C-terminal fimbrial subunit. The donor strand is then connected to a cholera toxin A2 (CTA2) subunit. The polypeptide sequences of one of the examples is as in SEQ ID No. 43, which is encoded by the nucleotide sequence of SEQ ID Nos. 42. In this example, the N-terminal subunit is CssA, with the N-terminal 15 amino acids of the mature CssA sequence deleted. In this example, a pelB leader sequence (22 amino acids) was also added, which is illustrated in FIG. 14.

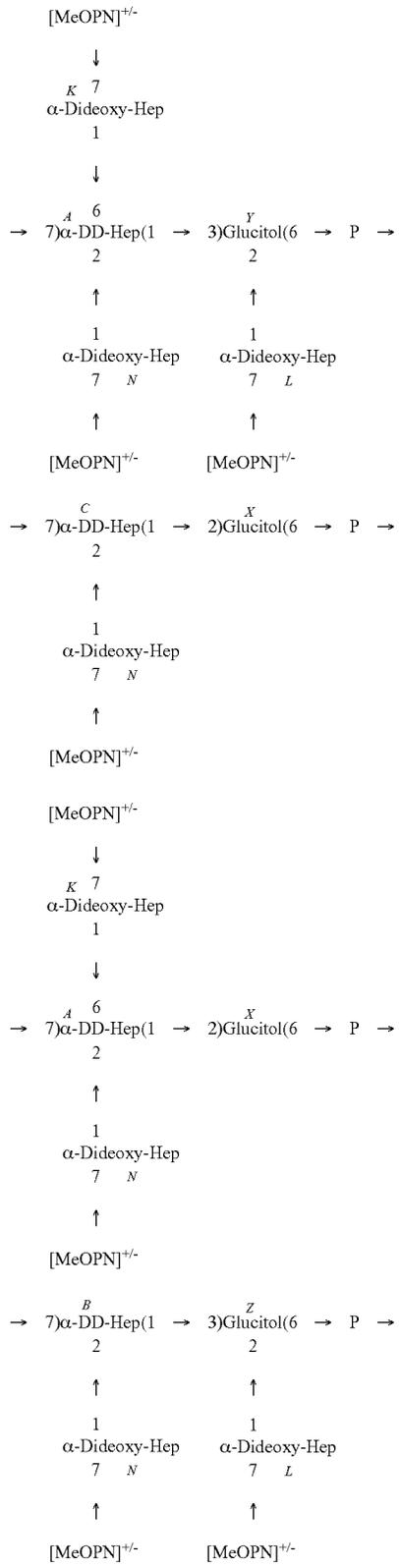
#### Example 3: *C. jejuni* Capsule Polysaccharides

Recent development of a molecular CPS typing system re-enforced the strong correlation between CPS and Penner types (Poly, et al., J. Clin. Microbiol. 49: 1750 (2011)). Both Penner serotyping and molecular CPS typing have revealed the predominance of a handful of CPS types worldwide. Also, despite over 60 Penner serotypes having been identified, most *Campylobacter* diarrheal disease is caused by *C. jejuni* expressing only a limited number of serotypes. Therefore, only selected strains of *C. jejuni*, predicated on epidemiological studies, provides suitable candidate strains for development of vaccine compositions. However, despite the importance of this organism to human disease, there are no licensed vaccines against *C. jejuni*.



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Additionally, the capsule polysaccharide from the HS5 strain of *C. jejuni* can be attached. HS 5 contains a complex of variations of polysaccharides. These include the following structures:



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Example 4: Induction of Immune Response by ETEC-Campylobacter Capsule Conjugates

i 5 Induction of an immune response by the conjugates was evaluated. In these studies, BALB/c mice were immunized with escalating amounts of vaccines administered with Alhydrogel® (Sergent Adjuvants, Clifton, N.J.). Mice received a total of two immunization at a 4-week interval.

10 The results of these studies is illustrated in FIG. 4. As shown in FIG. 4, two weeks following the first immunization, mice immunized with HS36-CfaEB (10 µg, 60 µg) and HS36-CfaE (60 µg) exhibited significant levels of serum IgG antibodies specific against HS36 CPS (p<0.05) (see FIG. 4 15 (A)), compared to pre-immune sera. Following two immunizations all groups of immunized animals had antibody levels that were significant increased (p<0.05) compared to levels observed after only one immunization. This effect was not dose dependent at the vaccine doses tested.

20 Furthermore, as illustrated in FIG. 4 (B), antibodies against CfaE was also determined by ELISA. As shown in FIG. 4(B), all mice immunized with the conjugate vaccine possessed significant levels of anti-CfaE IgG (p<0.05) for CPS-CfaE or CPS CfaEB. No dose dependent effects were observed and all groups displayed similar levels of CfaE-specific IgG.

ii 25 The data shown in FIG. 4 illustrates that the conjugate vaccine comprising an ETEC adhesin-based carrier protein conjugated to a *C. jejuni* CPS is capable of inducing an immune response against both bacterial components, i.e., *C. jejuni* CPS and ETEC CfaE.

30 To determine the levels of functional anti-adhesive antibody generated by HS36 conjugate vaccines, serum samples were tested by hemagglutination inhibition assay (HAI) assay in order to measure functional anti-adhesive antibodies present in the immune mouse serum.

35 The HAI assays were conducted by evaluating samples from each animal. The samples were initially diluted 1:8, then diluted two-fold over a wide range of dilutions. Each serum dilution was incubated with an equal volume of CFA/I+ ETEC bacteria (strain H10407), which further 40 diluted the serum 1:2. The final lowest dilution tested was 1:16, which was the limit of detection (LOD). The pre-incubated mixture was subsequently mixed with bovine erythrocytes in the presence of 0.5% mannose in U-bottom 96-well plates. In the absence of anti-adhesive antibodies, 45 the erythrocytes formed visible agglutinated "buttons" of cells. In the presence of anti-adhesive antibodies, agglutination was inhibited. The HAI titer was the highest serial dilution that completely inhibited agglutination. If there was not detectable inhibition at the lowest serum dilution of 1:16, 50 the samples were assigned a value of one-half of the detection limit (i.e., 8) for computational purposes.

55 The results of the HAI analysis are illustrated in FIG. 5. Prior to immunization, pooled serum contained HAI titers below the assay's level of detection. Following immunization, all groups of mice displayed significantly (p<0.05) 60 higher levels of anti-adhesive antibodies in their sera compared to pre-immune titers. Generally, mice immunized with HS36-CfaEB conjugate vaccine exhibited higher HAI titers. However, the only significance difference (P<0.05) observed 65 was between mice immunized with an HS36-CfaEB (60 µg) and HS36-CfaE (10 µg).

### Example 5: Immune Response Against Multiple MeOPN-6-Gal

#### Synthesis of Polysaccharide Construct

A polysaccharide constructed was synthesized as shown in FIG. 6. Starting from a previously reported compound 4-methoxyphenyl- $\alpha$ -D-galactopyranoside (see also FIG. 7, structure 1) (Comfort, et al., Biochem. 46: 3319-3330 (2007)), trityl group was selectively introduced to C-6. Originally, benzylation was performed on compound (FIG. 7, structure 2), however extensive migration observed during the introduction of MeOPN lead us to look for a more suitable protecting group. Therefore, allyl groups were selected to protect the C-2, C-3 and C-4 positions which were resistant to migration. Allyl groups were later deprotected with catalytic hydrogenolysis which proved to be compatible with the MeOPN modification.

As shown in FIG. 6 and FIG. 7, after allyl groups were installed, an aminopentanyl linker was introduced to the anomeric position as a site for conjugation. Starting from galactoside (FIG. 7, structure 3), 4-methoxyphenyl group (OMP) was first removed with cerium ammonium nitrate (CAN). The corresponding hemiacetal was then converted into trichloroacetimidate donor. 5-Amino-N-phthalimidopentanyl linker was then introduced with TMSOTf as activator at 0° C. Compound 5 (FIG. 7) was collected with 65% as the  $\beta$  anomer and 29% as the  $\alpha$  anomer. The removal of trityl group gave a free 6-hydroxyl group for modification.

The strategy for the introduction of MeOPN group was inspired by a similar reaction initially proposed by C. Mara et al, Bioorg. Med. Chem. Lett. 6180-6183 (2011). Compound 6 (FIG. 6 and FIG. 7) was treated with commercially available methyl dichlorophosphate in the presence of triethyl amine, followed by ammonolysis. Due to the chirality nature of the newly introduced MeOPN (R and S), product 7 (FIG. 7, structure 7) was collected as a mixture of two diastereoisomers. <sup>1</sup>H NMR was able to confirm that product 7 (FIG. 7) was indeed a 1:1 mixture of two diastereoisomers, revealing two sets of signals throughout the spectrum, such can be seen for anomeric and O-Me signals. The reaction yielded a mixture of side products, the most abundant being the O-Me group being replaced by a second NH<sub>2</sub>, accounting for the poor yield of this reaction.

Allyl and phthalimido protecting groups were removed with palladium (II) chloride and hydrazine respectively, generating product 9 (FIG. 7, structure 9). Similar to compound 7 (FIG. 7), a mixture of diastereoisomers is apparent in NMR. Although not optically pure, the <sup>31</sup>P NMR result agrees with native MeOPN-containing polysaccharides, having a phosphorous signals around 14 ppm. <sup>31</sup>H-<sup>31</sup>P HMBC NMR experiment was able to confirm that the MeOPN was introduced to the O-6 position, showing correlation signal with O-Me as well as the H-6 signals.

#### Induction of Immunity Against MeOPN-6-Gal

In one embodiment, galactose modified at the 6 carbon with O-methyl phosphoramidate (MeOPN-6-Gal) is used to induce immunity against multiple *C. jejuni* strains, even those strains not expressing MeOPN-6-Gal. As illustrated in FIG. 8, the monosaccharide construct MeOPN-6-Gal was recognized by antibody against capsule polysaccharide isolated from HS23/36, conjugated to CRM<sub>197</sub>. Unexpectedly, antibody against polysaccharide from HS4, conjugated to CRM<sub>197</sub>, also elicited an equivalent response, as anti-HS23/36 CRM<sub>197</sub> conjugate, against MeOPN-6-Gal. Also, anti-HS1-CRM<sub>197</sub>, also reacted to MeOPN-6-Gal, although to a somewhat less extent.

The strong cross-reactivity with MeOPN-6-Gal exhibited against HS23/36 and HS4 antibody may be explained by the fact that MeOPN-6-Gal share epitopic structures with HS23/36 and HS4 capsule polysaccharides. One explanation may be that the MeOPN group in both HS23/36 and HS4 is to a primary hydroxyl. The cross reaction of MeOPN-6-Gal (HS23/36) with HS4, which contains MeOPN-7-6d- $\beta$ -D-ido-Heptose, was unexpected, but may be due to the linkage of MeOPN to primary hydroxyl positions on both sugars. This feature is illustrated in FIG. 8 by the arrow.

### Example 6: Immunogenic Composition Against *C. jejuni* and Enterotoxigenic *Escherichia coli* (ETEC) Using a Combined *C. jejuni* Capsule/ETEC Construct

A synthetic conjugate vaccine strategy can be developed to protect against multiple enteric pathogens. Most efforts at development of vaccines against bacterial enteric pathogens are limited to a specific pathogen. The ability to combine vaccines against multiple, antigenically variable pathogens in a single, multi-valent, injectable vaccine would greatly simplify approaches to prevent acquisition and transmission of these pathogens worldwide. Globally, ETEC and *C. jejuni* are among the leading causes of bacterial diarrheal disease. In addition CJ has been causally linked to several serious sequelae including Guillain Barré Syndrome, irritable bowel syndrome, and reactive arthritis. Moreover, recent studies have indicated an association between CJ infections and malnutrition and growth stunting in young children in resource-limited settings.

Using conventional methods, we have developed conjugate vaccines containing CJ polysaccharide capsules that have proven to be immunogenic in multiple animal species and to confer protection against *C. jejuni* diarrhea in NHP. The newer synthetic approach is based on recent data that the immunodominant epitope on CJ polysaccharide capsule conjugate vaccines is the MeOPN modification found on different sugars in different capsule types.

Therefore, an immunogenic platform against both *C. jejuni* and ETEC can be created by linking synthetic MeOPN-sugars to different ETEC protein antigens. The approach could also be extended to include *Shigella* lipopolysaccharides (synthetic or detoxified) conjugated to ETEC proteins. Thus, this platform could form the basis of a multivalent vaccine against three major bacterial diarrheal pathogens. Conjugation can also serve as a protein carrier to enhance immunogenicity of the *Campylobacter* construct.

It is envisioned to conjugate the construct of Examples 3-5 to an ETEC construct. The overall method of conjugating includes oxidizing *C. jejuni* CPS, for example, with NaIO<sub>4</sub> in sodium acetate (pH 4.0). Oxidized CPSs were desalted with a 5 kDa cutoff membrane by stirred ultrafiltration, which is subsequently lyophilized. ETEC proteins are then added. The stoichiometry protein to CPS can vary, however, a typical ratio is 1:2 protein to CPS by mass. The concentration of components can be by any method. However, for example, polysaccharide concentration was determined by anthrone assay and protein concentration was determined by Pierce 660 protein assay or the BCA assay. NaCNBH<sub>3</sub> is then added. The conjugates can then be subsequently desalted by ultrafiltration and lyophilized. CPS, ETEC proteins and conjugates were analyzed, for example by SEC-HPLC or by SDS polyacrylamide gel electrophoresis (PAGE), or other methods.

### Example 7: Non-Human Primate Response

The immunogenicity of CfaE-HS23/36 and CfaEB-HS23/36 conjugates was observed in mice, as well as induction of

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hemagglutination inhibition (HAI) titers against CfaI in mice. The amino acid sequence of the dscCfaE construct used is SEQ ID No. 138 (nucleotide sequence is SEQ ID No. 139). The dsc<sub>19</sub>CfaE amino acid sequence is SEQ ID No. 143 (nucleotide sequence is SEQ ID No. 142). The amino acid sequence for dsc<sub>19</sub>CfaEB is SEQ ID No. 141 (nucleotide sequence is SEQ ID No. 140).

The CfaEB-HS23/36 conjugate was down-selected in order to proceed to studies in *Aotus nancymae*. This non-human primate (NHP) model was selected because it has been used as a diarrheal disease model for both ETEC and *C. jejuni*. We synthesized a lot of the CfaEB-HS23/36 vaccine that was sufficient in size for three NHP studies by reductive amination. The first such study, which is the only one that has been completed, was a dose finding study followed by a *C. jejuni* challenge.

The design of this NHP study is shown in Table 7. Animals (6 per group) were immunized three times at days 0, 42, and 84. The CfaEB-HS23/36 vaccine was given subcutaneously at either 0.5 ug or 3.5 ug polysaccharide (PS) adjuvanted with aluminum hydroxide. The ratio of PS to protein in the vaccine was roughly 1:1 so this was equivalent to 0.5 or 3.5 ug of CfaEB per dose. The 3.5 ug dose was also given intradermally (ID) with poly-IC as adjuvant. This was done to bridge to previous work done using ID immunizations with CfaEB alone. Similarly, another group was given HS23/36-CRM197 subcutaneously to bridge to previous work with the same capsule conjugated to another protein. Finally, the control group was immunized with PBS. On day 148 the animals were all challenged with 4x10<sup>11</sup> CFU of CG8421, an HS23/36 strain.

TABLE 7

Design of NHP study						
Group	Route	CfaEB-CPS	CPS-CRM197	Alum (ug)	Poly IC (ug)	PBS
1	SC	0.5	-	300	-	-
2	SC	3.5	-	300	-	-
3	ID	3.5	-	-	100	-
4	SC	-	3.5	300	-	-
5	SC	-	-	-	-	+

Animals were observed for diarrheal disease daily for 10 days following challenge. Diarrhea was defined as two or more days of consecutive stools that were ≥grade 3. The results are summarized in Table 8. Only 3/5 animals in the PBS group developed diarrhea for an attack rate of 60%. Note that one animal was eliminated because it developed diarrhea prior to challenge. The mean time to onset of disease in this negative control group was 2.3 days and the mean duration of illness was 5.3 days. The attack rate in the animals immunized with the HS23/36-CRM197 vaccine was 33% (2/6), with a mean onset of disease of 2 days and a mean duration of illness of 4 days (45% efficacy). Animals that were immunized with CfaEB-HS23/36 intradermally with poly IC also showed an attack rate of 33% with a mean onset of 1.5 days and a duration of two days (45% efficacy). The animals immunized subcutaneously with CfaEB-CPS showed between 67-100% efficacy against diarrheal disease. The attack rate in the group immunized with 0.5 ug of the vaccine was 0 (0/5, with one animal that vomited after challenge being eliminated) and the attack rate in the group immunized with 3.5 ug of the vaccine was 20% (1/5, with one animal being eliminated due to diarrhea prior to challenge). The single animal in this group that did develop

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diarrhea had a later onset of disease (day 9). There were no significant differences among the control group and any of the immunized animals due to the small numbers of animals per group.

TABLE 8

Results of challenge with <i>C. jejuni</i> CG8421.						
Group	Vaccine	#ill/total	Attack rate (%)	Mean days to onset of diarrhea (range)	Mean days of illness (range)	Protective efficacy
1	CfaEB-CPS (0.5 ug) + alum	0/5*	0	0	0	100
2	CfaEB-CPS (3.5 ug) + alum	1/5**	20	9	2	67
3	CfaEB-CPS (3.5 ug) + poly IC	2/6	33	1.5 (1-4)	2 (2-4)	45
4	CRM-CPS + alum	2/6	33	2 (1-3)	4 (2-6)	45
5	PBS	3/5**	60	2.3 (1-6)	5.3 (2-10)	—

\*One animal vomited after challenge and was excluded

\*\*Animals were excluded from analyses due to diarrheal onset prior to challenge

Serology results are shown in FIG. 9. Immune responses to CPS and to CfaE were measured by ELISA. Animals in groups 1, 2 and 3 displayed IgG responses to both antigens and IgA response to CfaE. Hemagglutination inhibition (HAI) titers against ETEC strain H10407 expressing CfaI fimbriae were determined and are shown in FIG. 10. The results indicate that HAI titers were detected in animals in groups 1, 2 and 3, with group 2 showing the highest titers.

#### Example 8: Synthesis and Immunogenicity of Additional Combinations of ETEC-*Campylobacter* Capsule Conjugates

CssBA-HS3 vaccine. CssBA is a recombinant form of the two subunits of CS6 that are fused together. This protein was conjugated to capsule from an HS3 strain by TEMPO oxidation. The conjugates were analyzed by SDS-PAGE and immunoblotting. Purified CssBA has a predicted Mr of 31.8 kDa. The conjugate of CssBA-HS3 CPS runs as two bands, one slightly smaller than CssBA and one that runs at approximately 60 kDa. The bands in the conjugate react with both anti-CssBA antiserum and antibodies to whole cells of HS3, indicating that polysaccharide has been conjugated to the protein.

Mice were immunized subcutaneously with three doses of the vaccine given at 4 week intervals. Doses were 5 ug by weight or 25 ug by weight. Animals were bled at day 0 and two weeks after each immunization and the response to CssBA and to CPS were determined by ELISA. The results, shown in FIG. 11, indicate that there was a robust response to both the protein and the polysaccharide at both doses.

#### LTB-HS4 Vaccine.

LTB is the binding component of the heat labile enterotoxin of ETEC. Recombinant LTB, which is not toxic, was conjugated to the polysaccharide capsule of an HS4 strain by reductive amination. The conjugate was analyzed by immunoblotting as shown in FIG. 12. Immunodetection with anti-LTB antiserum revealed a single band for LTB at approximately 10 kDa. The conjugate contained 4 major bands ranging from ~20 kDa→75 kDa that were reactive with both anti-LTB and anti-HS4 antiserum, indicating successful conjugation.

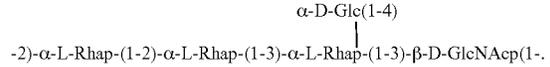
Mice were immunized with three doses of either 5 or 25 ug (by weight) of the LTB-HS4 conjugate subcutaneously at 4 week intervals and the serum immune response was determined. The results, shown in FIG. 12, indicate that there was a robust immune response to both the HS4 capsule and to LTB at both doses.

Example 9: Conjugation to *Shigella*  
Lipopolysaccharide (LPS)

There are four species of *Shigella*, a human pathogen cause diseases such as diarrhea and bacillary dysentery: *Shigella dysenteriae*, *Shigella flexneri*, *Shigella boydii* and *Shigella sonnei* are important enteropathogens. Strains of *Shigella* spp. Express long-chain lipopolysaccharides. The

chemical structures for many strains has been determined (see Liu, et al., FEMS Microbiol. Rev. 32: 627-653 (2008)).

An object of this invention, is a *Shigella* LPS-ETEC construct. The construct comprises an ETEC construct, as the above examples, conjugated, to a *Shigella* LPS, as an alternative or in addition to *C. jejuni* capsule polysaccharide. It is envisioned that any of the *Shigella* spp. can be conjugated to the ETEC construct. As an example, the *Shigella flexneri* 2a LPS is illustrated, as a potential LPS structure that can be conjugated to an ETEC construct, as follows:



SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 143

<210> SEQ ID NO 1

<211> LENGTH: 414

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 1

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20 25 30  
Ala Gly Thr Ala Thr Cys Ala Ala Cys Gly Ala Cys Thr Ala Thr Thr  
35 40 45  
Thr Cys Ala Ala Ala Ala Ala Gly Thr Thr Thr Thr Thr Thr Thr Gly  
50 55 60  
Cys Gly Cys Cys Thr Gly Ala Ala Cys Cys Ala Cys Ala Ala Ala Thr  
65 70 75 80  
Cys Cys Ala Gly Cys Cys Thr Thr Cys Thr Thr Thr Thr Gly Gly Thr  
85 90 95  
Ala Ala Ala Ala Ala Thr Gly Thr Thr Gly Gly Ala Ala Ala Gly Gly  
100 105 110  
Ala Ala Gly Gly Ala Gly Ala Thr Thr Thr Ala Thr Thr Ala Thr Thr  
115 120 125  
Thr Ala Gly Thr Gly Thr Gly Ala Gly Cys Thr Thr Ala Ala Thr Thr  
130 135 140  
Gly Thr Thr Cys Cys Thr Gly Ala Ala Ala Ala Thr Gly Thr Ala Thr  
145 150 155 160  
Cys Cys Cys Ala Gly Gly Thr Ala Ala Cys Gly Gly Thr Cys Thr Ala  
165 170 175  
Cys Cys Cys Thr Gly Thr Thr Thr Ala Thr Gly Ala Thr Gly Ala Ala  
180 185 190  
Gly Ala Thr Thr Ala Thr Gly Gly Ala Thr Thr Ala Gly Gly Ala Cys  
195 200 205  
Gly Ala Cys Thr Cys Gly Thr Ala Ala Ala Thr Ala Cys Cys Gly Cys  
210 215 220  
Thr Gly Ala Thr Gly Ala Thr Thr Cys Cys Cys Ala Ala Thr Cys Ala  
225 230 235 240  
Ala Thr Ala Ala Thr Cys Thr Ala Cys Cys Ala Gly Ala Thr Thr Gly  
245 250 255

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Thr Thr Gly Ala Thr Gly Ala Thr Ala Ala Ala Gly Gly Gly Ala Ala  
 260 265 270

Ala Ala Ala Ala Ala Thr Gly Thr Thr Ala Ala Ala Gly Ala Thr  
 275 280 285

Cys Ala Thr Gly Gly Thr Ala Cys Ala Gly Ala Gly Gly Thr Thr Ala  
 290 295 300

Cys Gly Cys Cys Thr Ala Ala Thr Cys Ala Ala Cys Ala Ala Ala Thr  
 305 310 315 320

Ala Ala Cys Thr Thr Thr Thr Ala Ala Ala Gly Cys Gly Cys Thr Gly  
 325 330 335

Ala Ala Thr Thr Ala Thr Ala Cys Thr Ala Gly Cys Gly Gly Ala Gly  
 340 345 350

Ala Thr Ala Ala Ala Gly Ala Ala Ala Thr Ala Cys Cys Thr Cys Cys  
 355 360 365

Thr Gly Gly Gly Ala Thr Ala Thr Ala Thr Ala Ala Cys Gly Ala Thr  
 370 375 380

Cys Ala Gly Gly Thr Thr Ala Thr Gly Gly Thr Thr Gly Gly Thr Thr  
 385 390 395 400

Ala Cys Thr Ala Thr Gly Thr Ala Ala Ala Cys Thr Ala Ala  
 405 410

<210> SEQ ID NO 2  
 <211> LENGTH: 137  
 <212> TYPE: PRT  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 2

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Ser Lys Ser Phe Phe Ala Pro Glu Pro Gln Ile Gln Pro Ser Phe Gly  
 20 25 30

Lys Asn Val Gly Lys Glu Gly Asp Leu Leu Phe Ser Val Ser Leu Ile  
 35 40 45

Val Pro Glu Asn Val Ser Gln Val Thr Val Tyr Pro Val Tyr Asp Glu  
 50 55 60

Asp Tyr Gly Leu Gly Arg Leu Val Asn Thr Ala Asp Asp Ser Gln Ser  
 65 70 75 80

Ile Ile Tyr Gln Ile Val Asp Asp Lys Gly Lys Lys Met Leu Lys Asp  
 85 90 95

His Gly Thr Glu Val Thr Pro Asn Gln Gln Ile Thr Phe Lys Ala Leu  
 100 105 110

Asn Tyr Thr Ser Gly Asp Lys Glu Ile Pro Pro Gly Ile Tyr Asn Asp  
 115 120 125

Gln Val Met Val Gly Tyr Tyr Val Asn  
 130 135

<210> SEQ ID NO 3  
 <211> LENGTH: 444  
 <212> TYPE: PRT  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 3

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 1 5 10 15

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 20 25 30

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Ala Ala Ala Thr Gly Thr Ala Ala Ala Thr Ala Thr Thr Gly Ala Gly  
 35 40 45

Cys Ala Ala Ala Ala Thr Thr Thr Thr Ala Thr Thr Cys Cys Ala Gly  
 50 55 60

Ala Thr Ala Thr Thr Gly Ala Thr Thr Cys Cys Gly Cys Thr Gly Thr  
 65 70 75 80

Thr Cys Gly Thr Ala Thr Ala Ala Thr Ala Cys Cys Thr Gly Thr Thr  
 85 90 95

Ala Ala Thr Thr Ala Cys Gly Ala Thr Thr Cys Gly Gly Ala Thr Cys  
 100 105 110

Cys Gly Ala Ala Ala Cys Thr Gly Ala Ala Thr Thr Cys Ala Cys Ala  
 115 120 125

Gly Thr Thr Ala Thr Ala Thr Ala Cys Gly Gly Thr Thr Gly Ala Gly  
 130 135 140

Ala Thr Gly Ala Cys Gly Ala Thr Cys Cys Cys Thr Gly Cys Ala Gly  
 145 150 155 160

Gly Thr Gly Thr Ala Ala Gly Cys Gly Cys Ala Gly Thr Thr Ala Ala  
 165 170 175

Ala Ala Thr Cys Gly Thr Ala Cys Cys Ala Ala Cys Ala Gly Ala Thr  
 180 185 190

Ala Gly Thr Cys Thr Gly Ala Cys Ala Thr Cys Thr Thr Cys Thr Gly  
 195 200 205

Gly Ala Cys Ala Gly Cys Ala Gly Ala Thr Cys Gly Gly Ala Ala Ala  
 210 215 220

Gly Cys Thr Gly Gly Thr Thr Ala Ala Thr Gly Thr Ala Ala Ala Cys  
 225 230 235 240

Ala Ala Thr Cys Cys Ala Gly Ala Thr Cys Ala Ala Ala Ala Thr Ala  
 245 250 255

Thr Gly Ala Ala Thr Thr Ala Thr Thr Ala Thr Ala Thr Cys Ala Gly  
 260 265 270

Ala Ala Ala Gly Gly Ala Thr Thr Cys Thr Gly Gly Cys Gly Cys Thr  
 275 280 285

Gly Gly Thr Ala Ala Gly Thr Thr Thr Ala Thr Gly Gly Cys Ala Gly  
 290 295 300

Gly Gly Cys Ala Ala Ala Ala Ala Gly Gly Ala Thr Cys Cys Thr Thr  
 305 310 315 320

Thr Thr Cys Thr Gly Thr Cys Ala Ala Ala Gly Ala Gly Ala Ala Thr  
 325 330 335

Ala Cys Gly Thr Cys Ala Thr Ala Cys Ala Cys Ala Thr Thr Cys Thr  
 340 345 350

Cys Ala Gly Cys Ala Ala Thr Thr Thr Ala Thr Ala Cys Thr Gly Gly  
 355 360 365

Thr Gly Gly Cys Gly Ala Ala Thr Ala Cys Cys Cys Thr Ala Ala Thr  
 370 375 380

Ala Gly Cys Gly Gly Ala Thr Ala Thr Thr Cys Gly Thr Cys Thr Gly  
 385 390 395 400

Gly Thr Ala Cys Thr Thr Ala Thr Gly Cys Ala Gly Gly Ala Cys Ala  
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Thr Thr Thr Gly Ala Cys Thr Gly Thr Ala Thr Cys Ala Thr Thr Thr  
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Thr Ala Cys Ala Gly Cys Ala Ala Thr Thr Ala Ala  
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<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 4

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Gln Asn Phe Ile Pro Asp Ile Asp Ser Ala Val Arg Ile Ile Pro Val
          20          25          30
Asn Tyr Asp Ser Asp Pro Lys Leu Asn Ser Gln Leu Tyr Thr Val Glu
          35          40          45
Met Thr Ile Pro Ala Gly Val Ser Ala Val Lys Ile Val Pro Thr Asp
 50          55          60
Ser Leu Thr Ser Ser Gly Gln Gln Ile Gly Lys Leu Val Asn Val Asn
 65          70          75          80
Asn Pro Asp Gln Asn Met Asn Tyr Tyr Ile Arg Lys Asp Ser Gly Ala
          85          90          95
Gly Lys Phe Met Ala Gly Gln Lys Gly Ser Phe Ser Val Lys Glu Asn
          100         105         110
Thr Ser Tyr Thr Phe Ser Ala Ile Tyr Thr Gly Gly Glu Tyr Pro Asn
          115         120         125
Ser Gly Tyr Ser Ser Gly Thr Tyr Ala Gly His Leu Thr Val Ser Phe
          130         135         140

Tyr Ser Asn
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<210> SEQ ID NO 5
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli
    
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<400> SEQUENCE: 5

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<210> SEQ ID NO 6
<211> LENGTH: 2502
<212> TYPE: DNA
<213> ORGANISM: Escherichia coli
    
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<400> SEQUENCE: 6

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&lt;210&gt; SEQ ID NO 7

&lt;211&gt; LENGTH: 833

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Escherichia coli

&lt;400&gt; SEQUENCE: 7

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Phe Thr Phe Ala Val Ser Ala Asp Lys Asn Pro Gly Ser Glu Asn Met
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```

Thr Asn Thr Ile Gly Pro His Asp Arg Gly Gly Ser Ser Pro Ile Tyr
35            40            45

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Asn Ile Leu Asn Ser Tyr Leu Thr Ala Tyr Asn Gly Ser His His Leu

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Gly	Ala	Cys	Pro	Ser	Ser	Asp	Ala	Pro	Gly	Thr	Ala	Thr	Ile	Asp	Gly
				85					90					95	
Glu	Thr	Asn	Ile	Thr	Leu	Gln	Phe	Thr	Glu	Lys	Arg	Ser	Leu	Ile	Lys
			100					105						110	
Arg	Glu	Leu	Gln	Ile	Lys	Gly	Tyr	Lys	Gln	Phe	Leu	Phe	Lys	Asn	Ala
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Asn	Cys	Pro	Ser	Lys	Leu	Ala	Leu	Asn	Ser	Ser	His	Phe	Gln	Cys	Asn
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Arg	Glu	Gln	Ala	Ser	Gly	Ala	Thr	Leu	Ser	Leu	Tyr	Ile	Pro	Ala	Gly
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Glu	Leu	Asn	Lys	Leu	Pro	Phe	Gly	Gly	Val	Trp	Asn	Ala	Val	Leu	Lys
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Leu	Asn	Val	Lys	Arg	Arg	Tyr	Asp	Thr	Thr	Tyr	Gly	Thr	Tyr	Thr	Ile
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Asn	Ile	Thr	Val	Asn	Leu	Thr	Asp	Lys	Gly	Asn	Ile	Gln	Ile	Trp	Leu
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Asp	Ser	Lys	Glu	Leu	Val	Tyr	Thr	Leu	Ser	Leu	Leu	Leu	Ala	Gly	Lys
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Asn	Leu	Thr	Pro	Thr	Asn	Gly	Gln	Ala	Leu	Asn	Ile	Asn	Thr	Ala	Ser
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Leu	Glu	Thr	Asn	Trp	Asn	Arg	Ile	Thr	Ala	Val	Thr	Met	Pro	Glu	Ile
305				310							315				320
Ser	Val	Pro	Val	Leu	Cys	Trp	Pro	Gly	Arg	Leu	Gln	Leu	Asp	Ala	Lys
			325						330					335	
Val	Lys	Asn	Pro	Glu	Ala	Gly	Gln	Tyr	Met	Gly	Asn	Ile	Lys	Ile	Thr
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Phe	Thr	Pro	Ser	Ser	Gln	Thr	Leu	Asp	Asn	Lys	Gln	Val	Glu	Lys	Asn
		355					360						365		
Ile	Thr	Val	Thr	Ala	Ser	Val	Asp	Pro	Ala	Ile	Asp	Leu	Leu	Gln	Ala
		370				375					380				
Asp	Gly	Asn	Ala	Leu	Pro	Ser	Ala	Val	Lys	Leu	Ala	Tyr	Ser	Pro	Ala
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Ser	Lys	Thr	Phe	Glu	Ser	Tyr	Arg	Val	Met	Thr	Gln	Val	His	Thr	Asn
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Asp	Ala	Thr	Lys	Lys	Val	Ile	Val	Lys	Leu	Ala	Asp	Thr	Pro	Gln	Leu
			420					425						430	
Thr	Asp	Val	Leu	Asn	Ser	Thr	Val	Gln	Met	Pro	Ile	Ser	Val	Ser	Trp
		435					440						445		
Gly	Gly	Gln	Val	Leu	Ser	Thr	Thr	Ala	Lys	Glu	Phe	Glu	Ala	Ala	Ala
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Leu	Gly	Tyr	Ser	Ala	Ser	Gly	Val	Asn	Gly	Val	Ser	Ser	Ser	Gln	Glu
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 Gly Asn Tyr Ser Gly Val Val Ser Leu Val Met Thr Leu Gly Ser Asp  
 500 505 510  
 Asn Lys Gln Val Glu Lys Asn Ile Thr Val Thr Ala Ser Val Asp Pro  
 515 520 525  
 Ala Gly Thr Leu Ala Ile Asp Phe Thr Pro Ile Glu Asn Ile Tyr Val  
 530 535 540  
 Gly Ala Asn Tyr Gly Lys Asp Ile Gly Thr Leu Val Phe Thr Thr Asn  
 545 550 555 560  
 Asp Leu Thr Asp Ile Thr Leu Met Ser Ser Arg Ser Val Val Asp Gly  
 565 570 575  
 Arg Gln Thr Gly Phe Phe Thr Phe Met Asp Ser Ser Ala Thr Tyr Lys  
 580 585 590  
 Ile Ser Thr Lys Leu Gly Ser Ser Asn Asp Val Asn Ile Gln Glu Ile  
 595 600 605  
 Thr Gln Gly Ala Lys Ile Thr Pro Val Ser Gly Glu Lys Thr Leu Pro  
 610 615 620  
 Lys Lys Phe Thr Leu Lys Leu His Ala His Arg Ser Ser Ser Thr Val  
 625 630 635 640  
 Pro Gly Thr Tyr Thr Val Gly Leu Asn Val Thr Ser Asn Val Ile Asp  
 645 650 655  
 Asn Lys Gln Ala Ala Gly Pro Thr Leu Thr Lys Glu Leu Ala Leu Asn  
 660 665 670  
 Val Leu Ser Pro Ala Ala Leu Asp Ala Thr Trp Ala Pro Gln Asp Asn  
 675 680 685  
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 690 695 700  
 Thr Leu Ser Asn Thr Ser Ile Asp Thr Val Ser Ile Ala Ser Thr Asn  
 705 710 715 720  
 Val Ser Asp Thr Ser Lys Asn Gly Thr Val Thr Phe Ala His Glu Thr  
 725 730 735  
 Asn Asn Ser Ala Ser Phe Ala Thr Thr Ile Ser Thr Asp Asn Ala Asn  
 740 745 750  
 Ile Thr Leu Asp Lys Asn Ala Gly Asn Thr Ile Val Lys Thr Thr Asn  
 755 760 765  
 Gly Ser Gln Leu Pro Thr Asn Leu Pro Leu Lys Phe Ile Thr Thr Glu  
 770 775 780  
 Gly Asn Glu His Leu Val Ser Gly Asn Tyr Arg Ala Asn Ile Thr Ile  
 785 790 795 800  
 Thr Ser Thr Ile Lys Asp Asn Lys Gln Ala Ala Gly Pro Thr Leu Thr  
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 820 825 830

His

<210> SEQ ID NO 8  
 <211> LENGTH: 3414  
 <212> TYPE: DNA  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 8

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accggaacgg cagggtgttc gaatagtaaa gaattagtaa ttggagcaac tacatccgga	1920
actgcaccaa gtgcaggtaa gtatcaaggc gtcgtttcca ttgtaatgac tcaatcgacc	1980
gacacagccg cgctgttcc tgacaataaa caagtagaga aaaatattac tgtgacagcc	2040
agtgttgatc ctactattga cattttgcaa gctgatggta gtagtttacc tactgctgta	2100
gaattaaact attcacctgc ggcaagtcgt tttgaaaatt ataaaatcgc aactaaagt	2160
catacaaatg ttataaataa aaatgtacta gtttaagctg taaatgatcc aaaacttaca	2220
aatgttttgg attctacaaa acaactcccc attactgtat catatggagg aaagactcta	2280
tcaaccgcag atgtgacttt tgaacctgca gaattaaatt ttggaacgctc aggtgtaact	2340
ggtgtatctt cttccaaga tttagtgatt ggtgcgacta cagcacaagc accaacggcg	2400
ggaaattata gtggggtcgt ttctatctta atgacctag catcagacaa taaacaagt	2460

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gaaaaaata tcaactgtaac agctagtggt gatcctacgg gcacattagc tattgatttt 2520
acgcctattg aaaatattta tgtaggtgcc aattatggta aagatattgg aacccttggt 2580
ttcacaacaa atgatttaac agatattaca ttgatgtcat ctgcagcgt tgttgatggt 2640
cgccagactg gtttttttac cttcatggac tcatcagcca cttacaaaat tagtacaaaa 2700
ctgggatcat cgaatgatgt aaacattcaa gaaattactc aaggagctaa aattactcct 2760
gttagtggag agaaaacttt gcctaaaaaa ttcactctta agctacatgc acacaggagt 2820
agcagtacag ttccaggtag gtatactggt ggtcttaacg taaccagtaa cgttattgat 2880
aacaagcagg cagcggggcc cactctaacc aaagaactgg cattaatgt gctttctcct 2940
gcagctctgg atgcaacttg ggctcctcag gataatttaa cattatccaa tactggcggt 3000
tctaataact tggtgggtgt tttgactctt tcaaatacca gtattgatac agttagcatt 3060
gagagtacaa atgtttctga tacatctaag aatggtacag taacttttgc acatgagaca 3120
aataactctg ctgactttgc caccaccatt tcaacagata atgccaacat tacgttggat 3180
aaaaatgctg gaaatacgat tgttaaaact acaaatggga gtcagttgcc aactaattta 3240
ccacttaagt ttattaccac tgaaggtaac gaacatttag tttcaggtaa ttaccgtgca 3300
aatataacaa ttacttcgac aattaagat aacaagcagg cggcagggcc aaccctgact 3360
aaggagttag cgctgaacgt tctgagcctc gagcaccacc accaccacca ctga 3414

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&lt;210&gt; SEQ ID NO 9

&lt;211&gt; LENGTH: 1137

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Escherichia coli

&lt;400&gt; SEQUENCE: 9

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Met Asn Lys Ile Leu Phe Ile Phe Thr Leu Phe Phe Ser Ser Gly Phe
1           5           10          15
Phe Thr Phe Ala Val Ser Ala Asp Lys Asn Pro Gly Ser Glu Asn Met
20          25          30
Thr Asn Thr Ile Gly Pro His Asp Arg Gly Gly Ser Ser Pro Ile Tyr
35          40          45
Asn Ile Leu Asn Ser Tyr Leu Thr Ala Tyr Asn Gly Ser His His Leu
50          55          60
Tyr Asp Arg Met Ser Phe Leu Cys Leu Ser Ser Gln Asn Thr Leu Asn
65          70          75          80
Gly Ala Cys Pro Ser Ser Asp Ala Pro Gly Thr Ala Thr Ile Asp Gly
85          90          95
Glu Thr Asn Ile Thr Leu Gln Phe Thr Glu Lys Arg Ser Leu Ile Lys
100         105         110
Arg Glu Leu Gln Ile Lys Gly Tyr Lys Gln Phe Leu Phe Lys Asn Ala
115         120         125
Asn Cys Pro Ser Lys Leu Ala Leu Asn Ser Ser His Phe Gln Cys Asn
130         135         140
Arg Glu Gln Ala Ser Gly Ala Thr Leu Ser Leu Tyr Ile Pro Ala Gly
145         150         155         160
Glu Leu Asn Lys Leu Pro Phe Gly Gly Val Trp Asn Ala Val Leu Lys
165         170         175
Leu Asn Val Lys Arg Arg Tyr Asp Thr Thr Tyr Gly Thr Tyr Thr Ile
180         185         190
Asn Ile Thr Val Asn Leu Thr Asp Lys Gly Asn Ile Gln Ile Trp Leu
195         200         205

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Pro Gln Phe Lys Ser Asn Ala Arg Val Asp Leu Asn Leu Arg Pro Thr  
 210 215 220  
 Gly Gly Gly Thr Tyr Ile Gly Arg Asn Ser Val Asp Met Cys Phe Tyr  
 225 230 235 240  
 Asp Gly Tyr Ser Thr Asn Ser Ser Ser Leu Glu Ile Arg Phe Gln Asp  
 245 250 255  
 Asp Asn Ser Lys Ser Asp Gly Lys Phe Tyr Leu Lys Lys Ile Asn Asp  
 260 265 270  
 Asp Ser Lys Glu Leu Val Tyr Thr Leu Ser Leu Leu Leu Ala Gly Lys  
 275 280 285  
 Asn Leu Thr Pro Thr Asn Gly Gln Ala Leu Asn Ile Asn Thr Ala Ser  
 290 295 300  
 Leu Glu Thr Asn Trp Asn Arg Ile Thr Ala Val Thr Met Pro Glu Ile  
 305 310 315 320  
 Ser Val Pro Val Leu Cys Trp Pro Gly Arg Leu Gln Leu Asp Ala Lys  
 325 330 335  
 Val Lys Asn Pro Glu Ala Gly Gln Tyr Met Gly Asn Ile Lys Ile Thr  
 340 345 350  
 Phe Thr Pro Ser Ser Gln Thr Leu Asp Asn Lys Gln Val Glu Lys Asn  
 355 360 365  
 Ile Thr Val Thr Ala Ser Val Asp Pro Ala Ile Asp Leu Leu Gln Ala  
 370 375 380  
 Asp Gly Asn Ala Leu Pro Ser Ala Val Lys Leu Ala Tyr Ser Pro Ala  
 385 390 395 400  
 Ser Lys Thr Phe Glu Ser Tyr Arg Val Met Thr Gln Val His Thr Asn  
 405 410 415  
 Asp Ala Thr Lys Lys Val Ile Val Lys Leu Ala Asp Thr Pro Gln Leu  
 420 425 430  
 Thr Asp Val Leu Asn Ser Thr Val Gln Met Pro Ile Ser Val Ser Trp  
 435 440 445  
 Gly Gly Gln Val Leu Ser Thr Thr Ala Lys Glu Phe Glu Ala Ala Ala  
 450 455 460  
 Leu Gly Tyr Ser Ala Ser Gly Val Asn Gly Val Ser Ser Ser Gln Glu  
 465 470 475 480  
 Leu Val Ile Ser Ala Ala Pro Lys Thr Ala Gly Thr Ala Pro Thr Ala  
 485 490 495  
 Gly Asn Tyr Ser Gly Val Val Ser Leu Val Met Thr Leu Gly Ser Asp  
 500 505 510  
 Asn Lys Gln Val Glu Lys Asn Ile Thr Val Thr Ala Ser Val Asp Pro  
 515 520 525  
 Thr Ile Asp Ile Leu Gln Ala Asn Gly Ser Ala Leu Pro Thr Ala Val  
 530 535 540  
 Asp Leu Thr Tyr Leu Pro Gly Ala Lys Thr Phe Glu Asn Tyr Ser Val  
 545 550 555 560  
 Leu Thr Gln Ile Tyr Thr Asn Asp Pro Ser Lys Gly Leu Asp Val Arg  
 565 570 575  
 Leu Val Asp Thr Pro Lys Leu Thr Asn Ile Leu Gln Pro Thr Ser Thr  
 580 585 590  
 Ile Pro Leu Thr Val Ser Trp Ala Gly Lys Thr Leu Ser Thr Ser Ala  
 595 600 605  
 Gln Lys Ile Ala Val Gly Asp Leu Gly Phe Gly Ser Thr Gly Thr Ala  
 610 615 620

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Gly Val Ser Asn Ser Lys Glu Leu Val Ile Gly Ala Thr Thr Ser Gly  
 625 630 635 640  
 Thr Ala Pro Ser Ala Gly Lys Tyr Gln Gly Val Val Ser Ile Val Met  
 645 650 655  
 Thr Gln Ser Thr Asp Thr Ala Ala Pro Val Pro Asp Asn Lys Gln Val  
 660 665 670  
 Glu Lys Asn Ile Thr Val Thr Ala Ser Val Asp Pro Thr Ile Asp Ile  
 675 680 685  
 Leu Gln Ala Asp Gly Ser Ser Leu Pro Thr Ala Val Glu Leu Thr Tyr  
 690 695 700  
 Ser Pro Ala Ala Ser Arg Phe Glu Asn Tyr Lys Ile Ala Thr Lys Val  
 705 710 715 720  
 His Thr Asn Val Ile Asn Lys Asn Val Leu Val Lys Leu Val Asn Asp  
 725 730 735  
 Pro Lys Leu Thr Asn Val Leu Asp Ser Thr Lys Gln Leu Pro Ile Thr  
 740 745 750  
 Val Ser Tyr Gly Gly Lys Thr Leu Ser Thr Ala Asp Val Thr Phe Glu  
 755 760 765  
 Pro Ala Glu Leu Asn Phe Gly Thr Ser Gly Val Thr Gly Val Ser Ser  
 770 775 780  
 Ser Gln Asp Leu Val Ile Gly Ala Thr Thr Ala Gln Ala Pro Thr Ala  
 785 790 795 800  
 Gly Asn Tyr Ser Gly Val Val Ser Ile Leu Met Thr Leu Ala Ser Asp  
 805 810 815  
 Asn Lys Gln Val Glu Lys Asn Ile Thr Val Thr Ala Ser Val Asp Pro  
 820 825 830  
 Thr Gly Thr Leu Ala Ile Asp Phe Thr Pro Ile Glu Asn Ile Tyr Val  
 835 840 845  
 Gly Ala Asn Tyr Gly Lys Asp Ile Gly Thr Leu Val Phe Thr Thr Asn  
 850 855 860  
 Asp Leu Thr Asp Ile Thr Leu Met Ser Ser Arg Ser Val Val Asp Gly  
 865 870 875 880  
 Arg Gln Thr Gly Phe Phe Thr Phe Met Asp Ser Ser Ala Thr Tyr Lys  
 885 890 895  
 Ile Ser Thr Lys Leu Gly Ser Ser Asn Asp Val Asn Ile Gln Glu Ile  
 900 905 910  
 Thr Gln Gly Ala Lys Ile Thr Pro Val Ser Gly Glu Lys Thr Leu Pro  
 915 920 925  
 Lys Lys Phe Thr Leu Lys Leu His Ala His Arg Ser Ser Ser Thr Val  
 930 935 940  
 Pro Gly Thr Tyr Thr Val Gly Leu Asn Val Thr Ser Asn Val Ile Asp  
 945 950 955 960  
 Asn Lys Gln Ala Ala Gly Pro Thr Leu Thr Lys Glu Leu Ala Leu Asn  
 965 970 975  
 Val Leu Ser Pro Ala Ala Leu Asp Ala Thr Trp Ala Pro Gln Asp Asn  
 980 985 990  
 Leu Thr Leu Ser Asn Thr Gly Val Ser Asn Thr Leu Val Gly Val Leu  
 995 1000 1005  
 Thr Leu Ser Asn Thr Ser Ile Asp Thr Val Ser Ile Ala Ser Thr  
 1010 1015 1020  
 Asn Val Ser Asp Thr Ser Lys Asn Gly Thr Val Thr Phe Ala His  
 1025 1030 1035  
 Glu Thr Asn Asn Ser Ala Ser Phe Ala Thr Thr Ile Ser Thr Asp

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1040	1045	1050
Asn Ala Asn Ile Thr Leu Asp Lys Asn Ala Gly Asn Thr Ile Val		
1055	1060	1065
Lys Thr Thr Asn Gly Ser Gln Leu Pro Thr Asn Leu Pro Leu Lys		
1070	1075	1080
Phe Ile Thr Thr Glu Gly Asn Glu His Leu Val Ser Gly Asn Tyr		
1085	1090	1095
Arg Ala Asn Ile Thr Ile Thr Ser Thr Ile Lys Asp Asn Lys Gln		
1100	1105	1110
Ala Ala Gly Pro Thr Leu Thr Lys Glu Leu Ala Leu Asn Val Leu		
1115	1120	1125
Ser Leu Glu His His His His His His		
1130	1135	

<210> SEQ ID NO 10  
 <211> LENGTH: 2952  
 <212> TYPE: DNA  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 10

```

atgaaaaaga tatttatttt ttgtctatc atattttctg cggtggtcag tgccgggcca      60
tacccgaaaa ctacagtagg taactctgacg aagagttttc aagcccctcg tcaggataga      120
agcgtacaat caccaatata taacatcttt acgaatcatg tggctggata tagtttgagt      180
cataacttat atgacaggat tgttttttta tgtacatcct cgtcgaatcc ggttaatggt      240
gcttgcccaa ccattggaac atctggagtt caatacggta ctacaacat aacctgcag      300
tttacagaaa aaagaagtct gataaaaaa aatattaatc ttgcaggtaa taagaaacca      360
atatgggaga atcagagttg cgacactagc aatctaattg tgttgaattc gaagtcttgg      420
tcctgtgggg cttacggaaa tgctaocgga acacttctaa atctgtatat cctgcagga      480
gaaatcaaca aattgccttt tggagggata tgggaggcaa ctctgatctt acgcttatca      540
agatatggcg aagtcagtag caccattac ggcaattata ccgtaaatat tacggttgat      600
ttaactgata aaggaatat tcaggtatgg cttccagggt ttcacagcaa cccgcgtgta      660
gacctgaatc tgcaccctat cgtaattat aaatatagtg gtagtaattc actcgacatg      720
tgtttctatg atggatatag tacaaacagt gatagcatgg taataaagt ccaggatgat      780
aatcctacct attcatctga atataatctt tataagatag gggcactga aaaattacc      840
tatgtgtttt cactgcttat gggagaaaa atattttatc cagtgaatgg tcaatcatt      900
actatcaatg acagtagtgt actcgaaca aactggaatc gagtaaccgc agttgctatg      960
ccggaagtta atgttccagt attatgctgg ccagcaagat tgctattaaa tgctgatgta     1020
aatgtcctcg atgcaggaca gtattcagga cagatatata taacatttac acccagtgtc     1080
gaaaatttag gcggtggagt cgaaaaaat attactgtga gggcaagtgt tgaccctaaa     1140
cttgatcttc tgcaagcaga tggaaactca ctgccggact ctatgcatt aacctattct     1200
tcggcttcaa ataatttga agtttactct cttaaactg ctattcatc aaatgacaaa     1260
agcaagggag ttgtagttaa gctgtcagct tcaccagttc tgtccaatat tatgaagcca     1320
aactcgcaaa ttccgatgaa agtgactttg ggggggaaga cgctgaatac aactgatact     1380
gagtttactg ttgatactct gaactttggt acatctgggt ttgaaaacgt ttcttccact     1440
caacagctta cgattcatgc agacacaaa ggaactgctc ctgaggcagg caattaccaa     1500
ggtattattt ctcttatcat gactcaaaaa acagggggcg gtgtcgaaaa aaatattact     1560
    
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gtgagggcaa gtgtcgacc taaacttgac cttctgcaat ctgatggctc tgcgctgccc 1620
aactctgtcg cattaaccta ttctccgct gtaaataatt ttgaagctca caccatcaac 1680
accgttgctc atacaaatga ctacagataa ggtgttgctg tgaagctgctc agcagatcca 1740
gtcctgtcca atgttctgaa tccaacctg caaatctctg tttctgtgaa tttcgcagga 1800
aaaccactga gcacaacagg cattaccatc gactccaatg atctgaactt tgcttcgagt 1860
ggtgttaata aagtttcttc tacgcagaaa ctttcaatcc atgcagatgc tactcgggta 1920
actggcggcg cactaacagc tggtaaatat cagggactcg tatcaattat cctgactaag 1980
tcaacggggg gcggtgtoga gaagaccatt agcgttacgg cgagtgttga cccgacgggc 2040
acattagcta ttgattttac gcctattgaa aatatttatg taggtgcca ttatggtaaa 2100
gatattgtaa ccctgtttt cacaacaaat gatttaacag atattacatt gatgtcatct 2160
cgcagcgttg ttgatggtcg ccagactggt tttttacct tcatggactc atcagccact 2220
tacaaaatta gtacaaaact gggatcatcg aatgatgtaa acattcaaga aattactcaa 2280
ggagctaaaa ttactcctgt tagtgagag aaaactttgc ctaaaaaatt cactcttaag 2340
ctacatgcac acaggagtag cagtacagtt ccaggtacgt atactgttgg tcttaacgta 2400
accagtaacg ttattgataa caagcaggca gcggggccca ctctaacca agaactggca 2460
ttaaatgtgc tttctctgc agctctggat gcaacttggg ctctcagga taatttaaca 2520
ttatccaata ctggcgtttc taacttttg gtgggtgttt tgactctttc aaataccagt 2580
attgatacag ttagcattgc gagtacaaat gtttctgata catctaagaa tggtagcagta 2640
acttttgac atgagacaaa taactctgct agctttgcca ccaccatttc aacagataat 2700
gccaacatta cgttgataa aaatgctgga aatacgattg ttaaaactac aaatgggagt 2760
cagttgcca ctaatttacc acttaagttt attaccactg aaggtaacga acatttagtt 2820
tcaggttaatt accgtgcaaa tataacaatt acttcgacaa ttaagataa caagcaggcg 2880
gcaggtccaa ccctgactaa ggagttagcg ctgaacgttc tgagcctcga gcaccaccac 2940
caccaccact ga 2952

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<210> SEQ ID NO 11
<211> LENGTH: 983
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

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<400> SEQUENCE: 11

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Met Lys Lys Ile Phe Ile Phe Leu Ser Ile Ile Phe Ser Ala Val Val
1           5           10          15
Ser Ala Gly Arg Tyr Pro Glu Thr Thr Val Gly Asn Leu Thr Lys Ser
20          25          30
Phe Gln Ala Pro Arg Gln Asp Arg Ser Val Gln Ser Pro Ile Tyr Asn
35          40          45
Ile Phe Thr Asn His Val Ala Gly Tyr Ser Leu Ser His Asn Leu Tyr
50          55          60
Asp Arg Ile Val Phe Leu Cys Thr Ser Ser Ser Asn Pro Val Asn Gly
65          70          75          80
Ala Cys Pro Thr Ile Gly Thr Ser Gly Val Gln Tyr Gly Thr Thr Thr
85          90          95
Ile Thr Leu Gln Phe Thr Glu Lys Arg Ser Leu Ile Lys Arg Asn Ile
100         105         110
Asn Leu Ala Gly Asn Lys Lys Pro Ile Trp Glu Asn Gln Ser Cys Asp

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Leu Thr Tyr Ser Pro Ala Val Asn Asn Phe Glu Ala His Thr Ile Asn  
 545 550 555 560  
 Thr Val Val His Thr Asn Asp Ser Asp Lys Gly Val Val Val Lys Leu  
 565 570 575  
 Ser Ala Asp Pro Val Leu Ser Asn Val Leu Asn Pro Thr Leu Gln Ile  
 580 585 590  
 Pro Val Ser Val Asn Phe Ala Gly Lys Pro Leu Ser Thr Thr Gly Ile  
 595 600 605  
 Thr Ile Asp Ser Asn Asp Leu Asn Phe Ala Ser Ser Gly Val Asn Lys  
 610 615 620  
 Val Ser Ser Thr Gln Lys Leu Ser Ile His Ala Asp Ala Thr Arg Val  
 625 630 635 640  
 Thr Gly Gly Ala Leu Thr Ala Gly Gln Tyr Gln Gly Leu Val Ser Ile  
 645 650 655  
 Ile Leu Thr Lys Ser Thr Gly Gly Gly Val Glu Lys Thr Ile Ser Val  
 660 665 670  
 Thr Ala Ser Val Asp Pro Thr Gly Thr Leu Ala Ile Asp Phe Thr Pro  
 675 680 685  
 Ile Glu Asn Ile Tyr Val Gly Ala Asn Tyr Gly Lys Asp Ile Gly Thr  
 690 695 700  
 Leu Val Phe Thr Thr Asn Asp Leu Thr Asp Ile Thr Leu Met Ser Ser  
 705 710 715 720  
 Arg Ser Val Val Asp Gly Arg Gln Thr Gly Phe Phe Thr Phe Met Asp  
 725 730 735  
 Ser Ser Ala Thr Tyr Lys Ile Ser Thr Lys Leu Gly Ser Ser Asn Asp  
 740 745 750  
 Val Asn Ile Gln Glu Ile Thr Gln Gly Ala Lys Ile Thr Pro Val Ser  
 755 760 765  
 Gly Glu Lys Thr Leu Pro Lys Lys Phe Thr Leu Lys Leu His Ala His  
 770 775 780  
 Arg Ser Ser Ser Thr Val Pro Gly Thr Tyr Thr Val Gly Leu Asn Val  
 785 790 795 800  
 Thr Ser Asn Val Ile Asp Asn Lys Gln Ala Ala Gly Pro Thr Leu Thr  
 805 810 815  
 Lys Glu Leu Ala Leu Asn Val Leu Ser Pro Ala Ala Leu Asp Ala Thr  
 820 825 830  
 Trp Ala Pro Gln Asp Asn Leu Thr Leu Ser Asn Thr Gly Val Ser Asn  
 835 840 845  
 Thr Leu Val Gly Val Leu Thr Leu Ser Asn Thr Ser Ile Asp Thr Val  
 850 855 860  
 Ser Ile Ala Ser Thr Asn Val Ser Asp Thr Ser Lys Asn Gly Thr Val  
 865 870 875 880  
 Thr Phe Ala His Glu Thr Asn Asn Ser Ala Ser Phe Ala Thr Thr Ile  
 885 890 895  
 Ser Thr Asp Asn Ala Asn Ile Thr Leu Asp Lys Asn Ala Gly Asn Thr  
 900 905 910  
 Ile Val Lys Thr Thr Asn Gly Ser Gln Leu Pro Thr Asn Leu Pro Leu  
 915 920 925  
 Lys Phe Ile Thr Thr Glu Gly Asn Glu His Leu Val Ser Gly Asn Tyr  
 930 935 940  
 Arg Ala Asn Ile Thr Ile Thr Ser Thr Ile Lys Asp Asn Lys Gln Ala  
 945 950 955 960

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Ala Gly Pro Thr Leu Thr Lys Glu Leu Ala Leu Asn Val Leu Ser Leu  
 965 970 975

Glu His His His His His His  
 980

<210> SEQ ID NO 12  
 <211> LENGTH: 2514  
 <212> TYPE: DNA  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 12

atgaaaaaag tgatttttgt tttatccatg tttctatggt ctcaggttta cgggcaatca 60  
 tggcatacga acgtagaggc tggttcaata aataaaacag agtcgatagg ccccatagac 120  
 cgaagtgctg ctgcatcgta tcttgctcat tataatattc atgaacatgt tgctggttac 180  
 aataaagatc actctctttt tgacaggatg acgtttttat gtatgtcatc aacagatgca 240  
 tctaaagggtg catgtccgac aggagaaaac tccaaatcct ctcaagggga gactaatatt 300  
 aagctaatat ttactgaaaa gaaaagtctg gccagaaaaa cattaactt aaaaggatat 360  
 aagagatttt tataatgaatc agatagatgc attcattatg tcgataaaat gaatctcaat 420  
 tctcatactg ttaaatgtgt aggttcattc acaagaggag tagatttcac tttatatatc 480  
 ccacaagggtg aaattgatgg gcttctaact ggaggtatat gggaggcaac actagagtta 540  
 cgagtcaaaa ggcattacga ctataatcat ggtacttaca aagttaatat cacagttgat 600  
 ttgacagaca aaggaaatat tcaggctcgg acaccaaagt ttcatagcga tctagaatt 660  
 gatctgaatt tacgtcctga aggtaatggt aaatattctg gtagtaacgt gcttgagatg 720  
 tgtctctatg atggctatag tacacatagt caaagtatag aaatgagggt tcaggatgac 780  
 tcacaaacag gaaataatga atataatcct ataaaaactg gagagccatt aaaaaaattg 840  
 ccataataaac tttctcttct tttaggagga cgagagtttt atccaaataa tggagaggct 900  
 tttactatta atgatacttc gtcattgttt ataaactgga atcgtattaa gtctgtatcc 960  
 ttaccacaga ttagtattcc agtactatgc tggccagcaa acttgacatt tatgtcagag 1020  
 ctaaataatc cagaagcggg tgagtattca ggaactta acgtaacatt tactcctagt 1080  
 agttcaagcc tagacaataa acaagccgag aaaaatatca ctgtaactgc tagcgttgat 1140  
 ccaactatcg atctgatgca atctgatggc acagcgttac caagtgcagt taatattgca 1200  
 tatcttcag gagagaaaag atttgaatct gctcgtatca ataccaagt tcataccaat 1260  
 aataaaaacta agggatttca gataaagctt actaatgata atgtggtaat gactaactta 1320  
 tctgatccaa gcaagactat tcttttagag gtttcattcg ctggcactaa gctgagcaca 1380  
 gctgcaacat ctattactgc cgatcaatta aatthtggcg cagctggtgt agagacagtt 1440  
 tctgcaacta aggaactcgt tattaatgca ggaagcacc agcaaaactaa tattgtagct 1500  
 ggtaactatc aaggattggt gtcaattgtg ctactcaag aacctgacaa taaacaagcc 1560  
 gagaaaaata tcaactgtaac tgctagcgtt gatccgacgg gcacattagc tattgatttt 1620  
 acgcctattg aaaatattta tgtaggtgcc aattatggtg aagatattgg aacccttgtt 1680  
 ttcacaacaa atgatttaac agatattaca ttgatgtcat ctcgcagcgt tgttgatggt 1740  
 cgccagactg gtttttttac cttcatggac tcatcagcca cttacaaaat tagtacaaaa 1800  
 ctgggatcat cgaatgatgt aaacattcaa gaaattactc aaggagctaa aattactcct 1860  
 gttagtggag agaaaacttt gcctaaaaaa ttcactctta agctacatgc acacaggagt 1920  
 agcagtacag tccagggtac gtatactggt ggtcttaacg taaccagtaa cgttattgat 1980

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aacaagcagg cagcggggcc cactctaacc aaagaactgg cattaatgt gctttctcct 2040
gcagctctgg atgcaacttg ggctctcag gataatttaa cattatccaa tactggcggt 2100
tctaatactt tgggtgggtgt tttgactctt tcaaatacca gtattgatac agttagcatt 2160
gcgagtacaa atgtttctga tacatctaag aatggtacag taacttttgc acatgagaca 2220
aataactctg ctagctttgc caccaccatt tcaacagata atgccaacat tacgttggat 2280
aaaaatgctg gaaatacagat tgtaaact acaaatggga gtcagttgcc aactaattha 2340
ccacttaagt ttattaccac tgaaggtaac gaacatttag tttcaggtaa ttaccgtgca 2400
aatataacaa ttacttcgac aattaaagat aacaagcagg cggcaggtcc aacctgact 2460
aaggagttag cgctgaacgt tctgagcctc gagcaccacc accaccacca ctga 2514

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<210> SEQ ID NO 13
<211> LENGTH: 837
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

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<400> SEQUENCE: 13

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Met Lys Lys Val Ile Phe Val Leu Ser Met Phe Leu Cys Ser Gln Val
 1          5          10         15
Tyr Gly Gln Ser Trp His Thr Asn Val Glu Ala Gly Ser Ile Asn Lys
 20          25          30
Thr Glu Ser Ile Gly Pro Ile Asp Arg Ser Ala Ala Ser Tyr Pro
 35          40          45
Ala His Tyr Ile Phe His Glu His Val Ala Gly Tyr Asn Lys Asp His
 50          55          60
Ser Leu Phe Asp Arg Met Thr Phe Leu Cys Met Ser Ser Thr Asp Ala
 65          70          75          80
Ser Lys Gly Ala Cys Pro Thr Gly Glu Asn Ser Lys Ser Ser Gln Gly
 85          90          95
Glu Thr Asn Ile Lys Leu Ile Phe Thr Glu Lys Lys Ser Leu Ala Arg
100         105         110
Lys Thr Leu Asn Leu Lys Gly Tyr Lys Arg Phe Leu Tyr Glu Ser Asp
115         120         125
Arg Cys Ile His Tyr Val Asp Lys Met Asn Leu Asn Ser His Thr Val
130         135         140
Lys Cys Val Gly Ser Phe Thr Arg Gly Val Asp Phe Thr Leu Tyr Ile
145         150         155         160
Pro Gln Gly Glu Ile Asp Gly Leu Leu Thr Gly Gly Ile Trp Glu Ala
165         170         175
Thr Leu Glu Leu Arg Val Lys Arg His Tyr Asp Tyr Asn His Gly Thr
180         185         190
Tyr Lys Val Asn Ile Thr Val Asp Leu Thr Asp Lys Gly Asn Ile Gln
195         200         205
Val Trp Thr Pro Lys Phe His Ser Asp Pro Arg Ile Asp Leu Asn Leu
210         215         220
Arg Pro Glu Gly Asn Gly Lys Tyr Ser Gly Ser Asn Val Leu Glu Met
225         230         235         240
Cys Leu Tyr Asp Gly Tyr Ser Thr His Ser Gln Ser Ile Glu Met Arg
245         250         255
Phe Gln Asp Asp Ser Gln Thr Gly Asn Asn Glu Tyr Asn Leu Ile Lys
260         265         270
Thr Gly Glu Pro Leu Lys Lys Leu Pro Tyr Lys Leu Ser Leu Leu Leu

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275					280					285					
Gly	Gly	Arg	Glu	Phe	Tyr	Pro	Asn	Asn	Gly	Glu	Ala	Phe	Thr	Ile	Asn
290						295				300					
Asp	Thr	Ser	Ser	Leu	Phe	Ile	Asn	Trp	Asn	Arg	Ile	Lys	Ser	Val	Ser
305				310						315					320
Leu	Pro	Gln	Ile	Ser	Ile	Pro	Val	Leu	Cys	Trp	Pro	Ala	Asn	Leu	Thr
				325					330					335	
Phe	Met	Ser	Glu	Leu	Asn	Asn	Pro	Glu	Ala	Gly	Glu	Tyr	Ser	Gly	Ile
			340					345					350		
Leu	Asn	Val	Thr	Phe	Thr	Pro	Ser	Ser	Ser	Ser	Leu	Asp	Asn	Lys	Gln
		355					360					365			
Ala	Glu	Lys	Asn	Ile	Thr	Val	Thr	Ala	Ser	Val	Asp	Pro	Thr	Ile	Asp
370					375						380				
Leu	Met	Gln	Ser	Asp	Gly	Thr	Ala	Leu	Pro	Ser	Ala	Val	Asn	Ile	Ala
385				390						395					400
Tyr	Leu	Pro	Gly	Glu	Lys	Arg	Phe	Glu	Ser	Ala	Arg	Ile	Asn	Thr	Gln
			405						410						415
Val	His	Thr	Asn	Asn	Lys	Thr	Lys	Gly	Ile	Gln	Ile	Lys	Leu	Thr	Asn
			420					425					430		
Asp	Asn	Val	Val	Met	Thr	Asn	Leu	Ser	Asp	Pro	Ser	Lys	Thr	Ile	Pro
		435					440					445			
Leu	Glu	Val	Ser	Phe	Ala	Gly	Thr	Lys	Leu	Ser	Thr	Ala	Ala	Thr	Ser
450					455						460				
Ile	Thr	Ala	Asp	Gln	Leu	Asn	Phe	Gly	Ala	Ala	Gly	Val	Glu	Thr	Val
465				470						475					480
Ser	Ala	Thr	Lys	Glu	Leu	Val	Ile	Asn	Ala	Gly	Ser	Thr	Gln	Gln	Thr
			485						490						495
Asn	Ile	Val	Ala	Gly	Asn	Tyr	Gln	Gly	Leu	Val	Ser	Ile	Val	Leu	Thr
			500					505					510		
Gln	Glu	Pro	Asp	Asn	Lys	Gln	Ala	Glu	Lys	Asn	Ile	Thr	Val	Thr	Ala
		515					520						525		
Ser	Val	Asp	Pro	Thr	Gly	Thr	Leu	Ala	Ile	Asp	Phe	Thr	Pro	Ile	Glu
530					535						540				
Asn	Ile	Tyr	Val	Gly	Ala	Asn	Tyr	Gly	Lys	Asp	Ile	Gly	Thr	Leu	Val
545				550						555					560
Phe	Thr	Thr	Asn	Asp	Leu	Thr	Asp	Ile	Thr	Leu	Met	Ser	Ser	Arg	Ser
			565						570						575
Val	Val	Asp	Gly	Arg	Gln	Thr	Gly	Phe	Phe	Thr	Phe	Met	Asp	Ser	Ser
			580					585					590		
Ala	Thr	Tyr	Lys	Ile	Ser	Thr	Lys	Leu	Gly	Ser	Ser	Asn	Asp	Val	Asn
		595					600						605		
Ile	Gln	Glu	Ile	Thr	Gln	Gly	Ala	Lys	Ile	Thr	Pro	Val	Ser	Gly	Glu
610					615						620				
Lys	Thr	Leu	Pro	Lys	Lys	Phe	Thr	Leu	Lys	Leu	His	Ala	His	Arg	Ser
625					630						635				640
Ser	Ser	Thr	Val	Pro	Gly	Thr	Tyr	Thr	Val	Gly	Leu	Asn	Val	Thr	Ser
			645						650						655
Asn	Val	Ile	Asp	Asn	Lys	Gln	Ala	Ala	Gly	Pro	Thr	Leu	Thr	Lys	Glu
			660						665					670	
Leu	Ala	Leu	Asn	Val	Leu	Ser	Pro	Ala	Ala	Leu	Asp	Ala	Thr	Trp	Ala
		675					680						685		
Pro	Gln	Asp	Asn	Leu	Thr	Leu	Ser	Asn	Thr	Gly	Val	Ser	Asn	Thr	Leu
690						695					700				

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Val Gly Val Leu Thr Leu Ser Asn Thr Ser Ile Asp Thr Val Ser Ile  
 705 710 715 720  
 Ala Ser Thr Asn Val Ser Asp Thr Ser Lys Asn Gly Thr Val Thr Phe  
 725 730 735  
 Ala His Glu Thr Asn Asn Ser Ala Ser Phe Ala Thr Thr Ile Ser Thr  
 740 745 750  
 Asp Asn Ala Asn Ile Thr Leu Asp Lys Asn Ala Gly Asn Thr Ile Val  
 755 760 765  
 Lys Thr Thr Asn Gly Ser Gln Leu Pro Thr Asn Leu Pro Leu Lys Phe  
 770 775 780  
 Ile Thr Thr Glu Gly Asn Glu His Leu Val Ser Gly Asn Tyr Arg Ala  
 785 790 795 800  
 Asn Ile Thr Ile Thr Ser Thr Ile Lys Asp Asn Lys Gln Ala Ala Gly  
 805 810 815  
 Pro Thr Leu Thr Lys Glu Leu Ala Leu Asn Val Leu Ser Leu Glu His  
 820 825 830  
 His His His His His  
 835

<210> SEQ ID NO 14  
 <211> LENGTH: 1845  
 <212> TYPE: DNA  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 14

atggcagtg gcccacgaa agatatgagt ttaggtgcaa atttaacttc agagcctaca 60  
 ttagctattg attttacgcc tattgaaaat atttatgtag gtgccaatta tggtaaagat 120  
 attggaacc ttgttttcac aacaaatgat ttaacagata ttacattgat gtcactctgc 180  
 agcgttgttg atggctgcca gactggtttt ttacacttca tggactcatc agccacttac 240  
 aaaattagta caaaactggg atcatcgaat gatgtaaaca ttcaagaaat tactcaagga 300  
 gctaaaatta ctctgttag tggagagaaa actttgccta aaaaattcac tcttaagcta 360  
 catgcacaca ggagtagcag tacagttcca ggtacgtata ctgttggctt taacgtaacc 420  
 agtaacgtta ttgataacaa gcaggcagcg gggcccactc taaccaaaga actggcatta 480  
 aatgtgcttt ctctgcagc tctggatgca acttgggctc ctcaggataa tttaacatta 540  
 tccaatactg gcgtttctaa tactttggtg ggtgttttga ctctttcaaa taccagtatt 600  
 gatacagtta gcattgcgag tacaatggt tctgatacat ctaagaatgg tacagtaact 660  
 tttgcacatg agacaaataa ctctgctagc tttgccacca ccatttcaac agataatgcc 720  
 aacattacgt tggataaaaa tgctggaat acgattgta aaactacaaa tgggagtcag 780  
 ttgccaaact atttaccact taagtttatt accactgaag gtaacgaaca tttagtttca 840  
 ggtaattacc gtgcaaatat aacaattact tcgacaatta aagataacaa gcaggcggca 900  
 ggtccaacc tgactaagga gttagcgtg aacgttttaa gcggtcaaa aagttttttt 960  
 gcacctgaac cacgaatata gccttctttt ggtgaaatg ttggaaagga aggagcttta 1020  
 ttatttagtg tgaacttaac tgttcctgaa aatgtatccc aggtaacggc ctaccctgtt 1080  
 tatgatgaag attatgggtt aggacgacta gtaaataccg ctgatgcttc ccaatcaata 1140  
 atctaccaga ttgttgatga gaaagggaaa aaaatgtaa aagatcatgg tgcagaggtt 1200  
 acacctaadc aacaataaac ttttaaagcg ctgaattata ctacggggga aaaaaaata 1260  
 tctctggaa tatataacga tcaggttatg gttggttact acgtcaacga caataaacia 1320

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ggaaactggc aatataaatc tctggatgta aatgtaaata ttgagcaaaa ttttattcca 1380
gatattgatt ccgctgttcg tataatacct gttaattacg attcggaccc gaaactggat 1440
tcacagttat atacggttga gatgacgatc cctgcagggtg taagcgcagt taaaatcgca 1500
ccaacagata gtctgacatc ttctggacag cagatcggaa agctgggttaa tgtaaacaaat 1560
ccagatcaaa atatgaatta ttatatcaga aaggattctg gcgctggtaa ctttatggca 1620
ggacaaaaag gatcctttcc tgtcaagag aatacgtcat acacattctc agcaatttat 1680
actggtggcg aatacctaa tagcggatat tegtctggta cttatgcagg aaatttgact 1740
gtatcatttt acagcaatga caataaaca agaacagaaa tagcgactaa aaacttccca 1800
gtatcaacga ctatttcact cgagcaccac caccaccacc actga 1845
    
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<210> SEQ ID NO 15
<211> LENGTH: 614
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli
    
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<400> SEQUENCE: 15

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Met Ala Val Gly Pro Thr Lys Asp Met Ser Leu Gly Ala Asn Leu Thr
1          5          10          15
Ser Glu Pro Thr Leu Ala Ile Asp Phe Thr Pro Ile Glu Asn Ile Tyr
20         25         30
Val Gly Ala Asn Tyr Gly Lys Asp Ile Gly Thr Leu Val Phe Thr Thr
35         40         45
Asn Asp Leu Thr Asp Ile Thr Leu Met Ser Ser Arg Ser Val Val Asp
50         55         60
Gly Arg Gln Thr Gly Phe Phe Thr Phe Met Asp Ser Ser Ala Thr Tyr
65         70         75         80
Lys Ile Ser Thr Lys Leu Gly Ser Ser Asn Asp Val Asn Ile Gln Glu
85         90         95
Ile Thr Gln Gly Ala Lys Ile Thr Pro Val Ser Gly Glu Lys Thr Leu
100        105        110
Pro Lys Lys Phe Thr Leu Lys Leu His Ala His Arg Ser Ser Ser Thr
115        120        125
Val Pro Gly Thr Tyr Thr Val Gly Leu Asn Val Thr Ser Asn Val Ile
130        135        140
Asp Asn Lys Gln Ala Ala Gly Pro Thr Leu Thr Lys Glu Leu Ala Leu
145        150        155        160
Asn Val Leu Ser Pro Ala Ala Leu Asp Ala Thr Trp Ala Pro Gln Asp
165        170        175
Asn Leu Thr Leu Ser Asn Thr Gly Val Ser Asn Thr Leu Val Gly Val
180        185        190
Leu Thr Leu Ser Asn Thr Ser Ile Asp Thr Val Ser Ile Ala Ser Thr
195        200        205
Asn Val Ser Asp Thr Ser Lys Asn Gly Thr Val Thr Phe Ala His Glu
210        215        220
Thr Asn Asn Ser Ala Ser Phe Ala Thr Thr Ile Ser Thr Asp Asn Ala
225        230        235        240
Asn Ile Thr Leu Asp Lys Asn Ala Gly Asn Thr Ile Val Lys Thr Thr
245        250        255
Asn Gly Ser Gln Leu Pro Thr Asn Leu Pro Leu Lys Phe Ile Thr Thr
260        265        270
Glu Gly Asn Glu His Leu Val Ser Gly Asn Tyr Arg Ala Asn Ile Thr
    
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275				280				285							
Ile	Thr	Ser	Thr	Ile	Lys	Asp	Asn	Lys	Gln	Ala	Ala	Gly	Pro	Thr	Leu
290					295						300				
Thr	Lys	Glu	Leu	Ala	Leu	Asn	Val	Leu	Ser	Gly	Ser	Lys	Ser	Phe	Phe
305					310					315					320
Ala	Pro	Glu	Pro	Arg	Ile	Gln	Pro	Ser	Phe	Gly	Glu	Asn	Val	Gly	Lys
				325					330					335	
Glu	Gly	Ala	Leu	Leu	Phe	Ser	Val	Asn	Leu	Thr	Val	Pro	Glu	Asn	Val
			340						345				350		
Ser	Gln	Val	Thr	Val	Tyr	Pro	Val	Tyr	Asp	Glu	Asp	Tyr	Gly	Leu	Gly
		355					360						365		
Arg	Leu	Val	Asn	Thr	Ala	Asp	Ala	Ser	Gln	Ser	Ile	Ile	Tyr	Gln	Ile
370						375					380				
Val	Asp	Glu	Lys	Gly	Lys	Lys	Met	Leu	Lys	Asp	His	Gly	Ala	Glu	Val
385					390					395					400
Thr	Pro	Asn	Gln	Gln	Ile	Thr	Phe	Lys	Ala	Leu	Asn	Tyr	Thr	Ser	Gly
				405					410					415	
Glu	Lys	Lys	Ile	Ser	Pro	Gly	Ile	Tyr	Asn	Asp	Gln	Val	Met	Val	Gly
			420						425				430		
Tyr	Tyr	Val	Asn	Asp	Asn	Lys	Gln	Gly	Asn	Trp	Gln	Tyr	Lys	Ser	Leu
		435					440						445		
Asp	Val	Asn	Val	Asn	Ile	Glu	Gln	Asn	Phe	Ile	Pro	Asp	Ile	Asp	Ser
450						455					460				
Ala	Val	Arg	Ile	Ile	Pro	Val	Asn	Tyr	Asp	Ser	Asp	Pro	Lys	Leu	Asp
465					470					475					480
Ser	Gln	Leu	Tyr	Thr	Val	Glu	Met	Thr	Ile	Pro	Ala	Gly	Val	Ser	Ala
				485					490					495	
Val	Lys	Ile	Ala	Pro	Thr	Asp	Ser	Leu	Thr	Ser	Ser	Gly	Gln	Gln	Ile
			500						505				510		
Gly	Lys	Leu	Val	Asn	Val	Asn	Asn	Pro	Asp	Gln	Asn	Met	Asn	Tyr	Tyr
		515					520						525		
Ile	Arg	Lys	Asp	Ser	Gly	Ala	Gly	Asn	Phe	Met	Ala	Gly	Gln	Lys	Gly
530						535					540				
Ser	Phe	Pro	Val	Lys	Glu	Asn	Thr	Ser	Tyr	Thr	Phe	Ser	Ala	Ile	Tyr
545					550					555					560
Thr	Gly	Gly	Glu	Tyr	Pro	Asn	Ser	Gly	Tyr	Ser	Ser	Gly	Thr	Tyr	Ala
				565					570					575	
Gly	Asn	Leu	Thr	Val	Ser	Phe	Tyr	Ser	Asn	Asp	Asn	Lys	Gln	Arg	Thr
				580					585				590		
Glu	Ile	Ala	Thr	Lys	Asn	Phe	Pro	Val	Ser	Thr	Thr	Ile	Ser	Leu	Glu
		595					600						605		
His	His	His	His	His											
610															

<210> SEQ ID NO 16  
 <211> LENGTH: 2487  
 <212> TYPE: DNA  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 16

atgaataaaa ttttatttat ttttacattg tttttttctt cagggttttt tacatttgcc 60  
 gtatcggcag ataaaaatcc cggaagtga aacatgacta atactattgg tccccatgac 120  
 agggggggat cttcccccat atataatc ttaaattcct atcttacagc atacaatgga 180

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agccatcatc tgtatgatag gatgagtttt ttatgtttgt cttctcaaaa taaactgaat	240
ggagcatgcc caagcagtgga tgcctcggc actgctacaa ttgatggcga aacaaatata	300
acattacaat ttacggaaaa aagaagtcta attaaaagag aactgcaaat taaaggctat	360
aaacaatttt tgttcaaaaa tgctaattgc ccatctaac tagcacttaa ctcatctcat	420
tttcaatgta atagagaaca agcttcagggt gctactttat cggtatacat accagctggg	480
gaattaaata aattaccttt tggggggggtc tgggaatgccg ttctgaagct aaatgtaaaa	540
agacgatatg atacaaccta tgggacttac actataaaca tcacagttaa ttaactgat	600
aagggaaata ttcagatgat gttaccacag ttcaaaaagta acgctcgtgt cgatcttaac	660
ttgcgtccaa ctgggtgggg tacatatatc ggaagaaatt ctggtgatat gtgcttttat	720
gatggatata gtactaacag cagctcttta gagataagat ttcaggatga taattctaaa	780
tctgatggaa aattttatct aaagaaaata aatgatgact ccaagaact tgtatacact	840
ttgtcacttc tcctggcagg taaaaattta acaccaacaa atggacaggc attaaatatt	900
aactctgctt ctctggaac aaactggaat agaattacag ctgtcacat gccagaatc	960
agtgttccgg tgttgtgttg gctcggacgt ttgcaattgg atgcaaaagt gaaaaatccc	1020
gaggtgggac aatatatggg gaattatata attactttca caccaagtag tcaaacactc	1080
gacaataaac aagtagagaa aaatattact gtaacagcta gtgttgatcc tgcaattgat	1140
cttttgcaag ctgatggcaa tgctctgcca tcagctgtaa agttagetta ttctcccgca	1200
tcaaaaactt ttgaaagtta cagagtaatg actcaagttc atacaaacga tgcaactaaa	1260
aaagtaattg ttaactctgc tgatacacca cagcttacag atgttctgaa ttcaactgtt	1320
caaatgccta tcagtgtgtc atggggagga caagtattat ctacaacagc caaagaattt	1380
gaagctgctg ctttgggata ttctgcatcc ggtgtaaatg gcgtatcatc ttctcaagag	1440
ttagtaatta gcgctgcacc taaaactgcc ggtaccgccc caactgcagg aaactattca	1500
ggagtagtat ctcttgaat gactttggga tccgacaata aacaagtaga gaaaaatatt	1560
actgtaacag ctagtgtoga cctcgcaggg aattttattc cagatattga ttccgctggt	1620
cgtataatc ctgttaatta cgattcggac ccgaaactgg attcacagtt atatacgggt	1680
gagatgacga tcctcgcagg tgtaagcgca gttaaaatcg caccaacaga tagtctgaca	1740
tcttctggac agcagatcgg aaagctgggt aatgtaaaaca atccagatca aaatagat	1800
tattatatca gaaaggattc tggcgtgggt aactttatgg caggacaaaa aggatccttt	1860
cctgtcaaaag agaatacgtc atacacattc tcagcaattt atactggtgg cgaataccct	1920
aatagcggat attcgtctgg tacttatgca ggaaatttga ctgtatcatt ttacagcaat	1980
gacaataaac aaagaacaga aatagcagct aaaaacttcc cagtatcaac gactatttca	2040
aaaagttttt ttgcacctga accacgaata cagccttctt ttggtgaaaa tgttgaaag	2100
gaaggagctt tattatttag tgtgaactta actgttctctg aaaatgtatc ccaggtaacg	2160
gtctaccctg tttatgatga agattatggg ttaggacgac tagtaaatc cgctgatgct	2220
tcccaatcaa taatctacca gattgttgat gagaaggga aaaaaatgtt aaaagatcat	2280
ggtgcagagg ttacacctaa tcaacaaata acttttaaag cgctgaatta tactagcggg	2340
gaaaaaaaaa tatctcctgg aatatataac gatcagggta tgggtgggta ctacgtaaac	2400
gacaataaac aacgtaccga gattgccacc aagaattttc cgggtgagcacc caccatcagc	2460
ctcgagcacc accaccacca cactga	2487

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<210> SEQ ID NO 17
<211> LENGTH: 828
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 17

Met Asn Lys Ile Leu Phe Ile Phe Thr Leu Phe Phe Ser Ser Gly Phe
 1           5           10           15
Phe Thr Phe Ala Val Ser Ala Asp Lys Asn Pro Gly Ser Glu Asn Met
 20           25           30
Thr Asn Thr Ile Gly Pro His Asp Arg Gly Gly Ser Ser Pro Ile Tyr
 35           40           45
Asn Ile Leu Asn Ser Tyr Leu Thr Ala Tyr Asn Gly Ser His His Leu
 50           55           60
Tyr Asp Arg Met Ser Phe Leu Cys Leu Ser Ser Gln Asn Thr Leu Asn
 65           70           75           80
Gly Ala Cys Pro Ser Ser Asp Ala Pro Gly Thr Ala Thr Ile Asp Gly
 85           90           95
Glu Thr Asn Ile Thr Leu Gln Phe Thr Glu Lys Arg Ser Leu Ile Lys
 100          105          110
Arg Glu Leu Gln Ile Lys Gly Tyr Lys Gln Phe Leu Phe Lys Asn Ala
 115          120          125
Asn Cys Pro Ser Lys Leu Ala Leu Asn Ser Ser His Phe Gln Cys Asn
 130          135          140
Arg Glu Gln Ala Ser Gly Ala Thr Leu Ser Leu Tyr Ile Pro Ala Gly
 145          150          155          160
Glu Leu Asn Lys Leu Pro Phe Gly Gly Val Trp Asn Ala Val Leu Lys
 165          170          175
Leu Asn Val Lys Arg Arg Tyr Asp Thr Thr Tyr Gly Thr Tyr Thr Ile
 180          185          190
Asn Ile Thr Val Asn Leu Thr Asp Lys Gly Asn Ile Gln Ile Trp Leu
 195          200          205
Pro Gln Phe Lys Ser Asn Ala Arg Val Asp Leu Asn Leu Arg Pro Thr
 210          215          220
Gly Gly Gly Thr Tyr Ile Gly Arg Asn Ser Val Asp Met Cys Phe Tyr
 225          230          235          240
Asp Gly Tyr Ser Thr Asn Ser Ser Ser Leu Glu Ile Arg Phe Gln Asp
 245          250          255
Asp Asn Ser Lys Ser Asp Gly Lys Phe Tyr Leu Lys Lys Ile Asn Asp
 260          265          270
Asp Ser Lys Glu Leu Val Tyr Thr Leu Ser Leu Leu Leu Ala Gly Lys
 275          280          285
Asn Leu Thr Pro Thr Asn Gly Gln Ala Leu Asn Ile Asn Thr Ala Ser
 290          295          300
Leu Glu Thr Asn Trp Asn Arg Ile Thr Ala Val Thr Met Pro Glu Ile
 305          310          315          320
Ser Val Pro Val Leu Cys Trp Pro Gly Arg Leu Gln Leu Asp Ala Lys
 325          330          335
Val Lys Asn Pro Glu Ala Gly Gln Tyr Met Gly Asn Ile Lys Ile Thr
 340          345          350
Phe Thr Pro Ser Ser Gln Thr Leu Asp Asn Lys Gln Val Glu Lys Asn
 355          360          365
Ile Thr Val Thr Ala Ser Val Asp Pro Ala Ile Asp Leu Leu Gln Ala
 370          375          380

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Asp Gly Asn Ala Leu Pro Ser Ala Val Lys Leu Ala Tyr Ser Pro Ala  
 385 390 395 400  
 Ser Lys Thr Phe Glu Ser Tyr Arg Val Met Thr Gln Val His Thr Asn  
 405 410 415  
 Asp Ala Thr Lys Lys Val Ile Val Lys Leu Ala Asp Thr Pro Gln Leu  
 420 425 430  
 Thr Asp Val Leu Asn Ser Thr Val Gln Met Pro Ile Ser Val Ser Trp  
 435 440 445  
 Gly Gly Gln Val Leu Ser Thr Thr Ala Lys Glu Phe Glu Ala Ala Ala  
 450 455 460  
 Leu Gly Tyr Ser Ala Ser Gly Val Asn Gly Val Ser Ser Ser Gln Glu  
 465 470 475 480  
 Leu Val Ile Ser Ala Ala Pro Lys Thr Ala Gly Thr Ala Pro Thr Ala  
 485 490 495  
 Gly Asn Tyr Ser Gly Val Val Ser Leu Val Met Thr Leu Gly Ser Asp  
 500 505 510  
 Asn Lys Gln Val Glu Lys Asn Ile Thr Val Thr Ala Ser Val Asp Pro  
 515 520 525  
 Ala Gly Asn Phe Ile Pro Asp Ile Asp Ser Ala Val Arg Ile Ile Pro  
 530 535 540  
 Val Asn Tyr Asp Ser Asp Pro Lys Leu Asp Ser Gln Leu Tyr Thr Val  
 545 550 555 560  
 Glu Met Thr Ile Pro Ala Gly Val Ser Ala Val Lys Ile Ala Pro Thr  
 565 570 575  
 Asp Ser Leu Thr Ser Ser Gly Gln Gln Ile Gly Lys Leu Val Asn Val  
 580 585 590  
 Asn Asn Pro Asp Gln Asn Met Asn Tyr Tyr Ile Arg Lys Asp Ser Gly  
 595 600 605  
 Ala Gly Asn Phe Met Ala Gly Gln Lys Gly Ser Phe Pro Val Lys Glu  
 610 615 620  
 Asn Thr Ser Tyr Thr Phe Ser Ala Ile Tyr Thr Gly Gly Glu Tyr Pro  
 625 630 635 640  
 Asn Ser Gly Tyr Ser Ser Gly Thr Tyr Ala Gly Asn Leu Thr Val Ser  
 645 650 655  
 Phe Tyr Ser Asn Asp Asn Lys Gln Arg Thr Glu Ile Ala Thr Lys Asn  
 660 665 670  
 Phe Pro Val Ser Thr Thr Ile Ser Lys Ser Phe Phe Ala Pro Glu Pro  
 675 680 685  
 Arg Ile Gln Pro Ser Phe Gly Glu Asn Val Gly Lys Glu Gly Ala Leu  
 690 695 700  
 Leu Phe Ser Val Asn Leu Thr Val Pro Glu Asn Val Ser Gln Val Thr  
 705 710 715 720  
 Val Tyr Pro Val Tyr Asp Glu Asp Tyr Gly Leu Gly Arg Leu Val Asn  
 725 730 735  
 Thr Ala Asp Ala Ser Gln Ser Ile Ile Tyr Gln Ile Val Asp Glu Lys  
 740 745 750  
 Gly Lys Lys Met Leu Lys Asp His Gly Ala Glu Val Thr Pro Asn Gln  
 755 760 765  
 Gln Ile Thr Phe Lys Ala Leu Asn Tyr Thr Ser Gly Glu Lys Lys Ile  
 770 775 780  
 Ser Pro Gly Ile Tyr Asn Asp Gln Val Met Val Gly Tyr Tyr Val Asn  
 785 790 795 800  
 Asp Asn Lys Gln Arg Thr Glu Ile Ala Thr Lys Asn Phe Pro Val Ser

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	805	810	815	
Thr Thr Ile Ser Leu Glu His His His His His His				
	820	825		
<p>&lt;210&gt; SEQ ID NO 18                  &lt;211&gt; LENGTH: 2490                  &lt;212&gt; TYPE: DNA                  &lt;213&gt; ORGANISM: Escherichia coli</p>				
<p>&lt;400&gt; SEQUENCE: 18</p>				
atgaataaaa ttttatttat ttttacattg tttttttctt caggggtttt tacatttgcc				60
gtatcggcag ataaaaatcc cggaagtga aacatgacta atactattgg tccccatgac				120
aggggggggat cttcccccat atataatc ttaaattcct atcttacagc atacaatgga				180
agccatcatc tgtatgatag gatgagtttt ttatgtttgt cttctcaaaa tacactgaat				240
ggagcatgcc caagcagtga tgcccctggc actgctacaa ttgatggcga aacaaatata				300
acattacaat ttacggaaaa aagaagtcta attaaaagag aactgcaaat taaaggctat				360
aaacaatttt tgttcaaaaa tgctaattgc ccatcctaac tagcaactaa ctcatctcat				420
tttcaatgta atagagaaca agcttcaggt gctactttat cgttatacat accagctggt				480
gaattaaata aattaccctt tggggggggtc tggaaatgcc ttctgaagct aaatgtaaaa				540
agacgatatg atacaacctt tgggacttac actataaaca tcacagttaa ttttaactgat				600
aagggaaata ttcagatatg gttaccacag ttcaaaagta acgctcgtgt cgatcttaac				660
ttgcgtccaa ctggtggtgg tacatatatc ggaagaaatt ctggtgatat gtgcttttat				720
gatggatata gtactaacag cagctcttta gagataagat ttcaggatga taattctaaa				780
tctgatggaa aattttatct aaagaaaata aatgatgact ccaaagaact tgtatacact				840
ttgtcacttc tcctggcagg taaaaattta acaccaaca atggacaggc attaaatatt				900
aaactgctt ctctggaac aaactggaat agaattacag ctgtcaccat gccagaaatc				960
agtgttccgg tgttgtgttg gcctggacgt ttgcaattgg atgcaaaagt gaaaaatccc				1020
gaggctggac aatatatggg gaattatata attacttca caccaagtag tcaaacactc				1080
gacaataaac aagtagagaa aaatattact gtaacagcta gtgttgatcc tgcaattgat				1140
cttttgcaag ctgatggcaa tgctctgcca tcagctgtaa agttagctta ttctcccgca				1200
tcaaaaactt ttgaaagtta cagagtaatg actcaagttc atacaaaaga tgcaactaaa				1260
aaagtattg ttaaacttgc tgatacacca cagcttacag atgttctgaa ttcaactggt				1320
caaatgccta tcagtgtgtc atggggagga caagtattat ctacaacagc caagaattt				1380
gaagctgctg ctttgggata ttctgcatcc ggtgtaaatg gcgtatcatc ttctcaagag				1440
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ggagtagtat ctcttgaat gactttggga tccgacaata aacaagtaga gaaaaatatt				1560
actgtaacag ctagtgtoga ccttgcaggg tcaaaaagtt tttttgcacc tgaaccacga				1620
atacagcctt cttttgtgta aaatgttga aaggaaggag ctttattatt tagtgtgaac				1680
ttaactgttc ctgaaaatgt atcccaggta acggtctacc ctgtttatga tgaagattat				1740
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gatgagaaag gaaaaaaat gttaaaagat catggtgcag aggttacacc taatcaacaa				1860
ataactttta aagcgtgtaa ttactatagc ggggaaaaaa aaatatctcc tggaatatat				1920
aacgatcagg ttatggttgg ttactacgtc aacgacaata aacaaggaaa ctggcaatat				1980

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aaatctctgg atgtaaagt aaatattgag caaaatttta ttccagatat tgattccgct 2040
gttcgtataa tacctgttaa ttacgattcg gaccogaaac tggattcaca gttatatacg 2100
gttgagatga cgatccctgc aggtgtaagc gcagttaaaa tcgcaccaac agatagtctg 2160
acatcttctg gacagcagat cggaaagctg gttaatgtaa acaatccaga tcaaaatatg 2220
aattattata tcagaaagga ttctggcgct ggtaacttta tggcaggaca aaaaggatcc 2280
tttctgtca aagagaatac gtcatacaca ttctcagcaa tttatactgg tggcgaatac 2340
cctaatacgc gatattcgtc tggtacttat gcaggaaatt tgactgtatc attttacagc 2400
aatgacaata aacaaggcaa ttggcagtac aagagcctcg acgtgaacgt gaacatcgaa 2460
cagctcgagc accaccacca ccaccactga 2490

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<210> SEQ ID NO 19
<211> LENGTH: 829
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

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<400> SEQUENCE: 19

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Met Asn Lys Ile Leu Phe Ile Phe Thr Leu Phe Phe Ser Ser Gly Phe
1           5           10          15
Phe Thr Phe Ala Val Ser Ala Asp Lys Asn Pro Gly Ser Glu Asn Met
20        25        30
Thr Asn Thr Ile Gly Pro His Asp Arg Gly Gly Ser Ser Pro Ile Tyr
35        40        45
Asn Ile Leu Asn Ser Tyr Leu Thr Ala Tyr Asn Gly Ser His His Leu
50        55        60
Tyr Asp Arg Met Ser Phe Leu Cys Leu Ser Ser Gln Asn Thr Leu Asn
65        70        75        80
Gly Ala Cys Pro Ser Ser Asp Ala Pro Gly Thr Ala Thr Ile Asp Gly
85        90        95
Glu Thr Asn Ile Thr Leu Gln Phe Thr Glu Lys Arg Ser Leu Ile Lys
100       105       110
Arg Glu Leu Gln Ile Lys Gly Tyr Lys Gln Phe Leu Phe Lys Asn Ala
115       120       125
Asn Cys Pro Ser Lys Leu Ala Leu Asn Ser Ser His Phe Gln Cys Asn
130       135       140
Arg Glu Gln Ala Ser Gly Ala Thr Leu Ser Leu Tyr Ile Pro Ala Gly
145       150       155       160
Glu Leu Asn Lys Leu Pro Phe Gly Gly Val Trp Asn Ala Val Leu Lys
165       170       175
Leu Asn Val Lys Arg Arg Tyr Asp Thr Thr Tyr Gly Thr Tyr Thr Ile
180       185       190
Asn Ile Thr Val Asn Leu Thr Asp Lys Gly Asn Ile Gln Ile Trp Leu
195       200       205
Pro Gln Phe Lys Ser Asn Ala Arg Val Asp Leu Asn Leu Arg Pro Thr
210       215       220
Gly Gly Gly Thr Tyr Ile Gly Arg Asn Ser Val Asp Met Cys Phe Tyr
225       230       235       240
Asp Gly Tyr Ser Thr Asn Ser Ser Ser Leu Glu Ile Arg Phe Gln Asp
245       250       255
Asp Asn Ser Lys Ser Asp Gly Lys Phe Tyr Leu Lys Lys Ile Asn Asp
260       265       270
Asp Ser Lys Glu Leu Val Tyr Thr Leu Ser Leu Leu Leu Ala Gly Lys
275       280       285

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Asn Leu Thr Pro Thr Asn Gly Gln Ala Leu Asn Ile Asn Thr Ala Ser  
 290 295 300  
 Leu Glu Thr Asn Trp Asn Arg Ile Thr Ala Val Thr Met Pro Glu Ile  
 305 310 315 320  
 Ser Val Pro Val Leu Cys Trp Pro Gly Arg Leu Gln Leu Asp Ala Lys  
 325 330 335  
 Val Lys Asn Pro Glu Ala Gly Gln Tyr Met Gly Asn Ile Lys Ile Thr  
 340 345 350  
 Phe Thr Pro Ser Ser Gln Thr Leu Asp Asn Lys Gln Val Glu Lys Asn  
 355 360 365  
 Ile Thr Val Thr Ala Ser Val Asp Pro Ala Ile Asp Leu Leu Gln Ala  
 370 375 380  
 Asp Gly Asn Ala Leu Pro Ser Ala Val Lys Leu Ala Tyr Ser Pro Ala  
 385 390 395 400  
 Ser Lys Thr Phe Glu Ser Tyr Arg Val Met Thr Gln Val His Thr Asn  
 405 410 415  
 Asp Ala Thr Lys Lys Val Ile Val Lys Leu Ala Asp Thr Pro Gln Leu  
 420 425 430  
 Thr Asp Val Leu Asn Ser Thr Val Gln Met Pro Ile Ser Val Ser Trp  
 435 440 445  
 Gly Gly Gln Val Leu Ser Thr Thr Ala Lys Glu Phe Glu Ala Ala Ala  
 450 455 460  
 Leu Gly Tyr Ser Ala Ser Gly Val Asn Gly Val Ser Ser Ser Gln Glu  
 465 470 475 480  
 Leu Val Ile Ser Ala Ala Pro Lys Thr Ala Gly Thr Ala Pro Thr Ala  
 485 490 495  
 Gly Asn Tyr Ser Gly Val Val Ser Leu Val Met Thr Leu Gly Ser Asp  
 500 505 510  
 Asn Lys Gln Val Glu Lys Asn Ile Thr Val Thr Ala Ser Val Asp Pro  
 515 520 525  
 Ala Gly Ser Lys Ser Phe Phe Ala Pro Glu Pro Arg Ile Gln Pro Ser  
 530 535 540  
 Phe Gly Glu Asn Val Gly Lys Glu Gly Ala Leu Leu Phe Ser Val Asn  
 545 550 555 560  
 Leu Thr Val Pro Glu Asn Val Ser Gln Val Thr Val Tyr Pro Val Tyr  
 565 570 575  
 Asp Glu Asp Tyr Gly Leu Gly Arg Leu Val Asn Thr Ala Asp Ala Ser  
 580 585 590  
 Gln Ser Ile Ile Tyr Gln Ile Val Asp Glu Lys Gly Lys Lys Met Leu  
 595 600 605  
 Lys Asp His Gly Ala Glu Val Thr Pro Asn Gln Gln Ile Thr Phe Lys  
 610 615 620  
 Ala Leu Asn Tyr Thr Ser Gly Glu Lys Lys Ile Ser Pro Gly Ile Tyr  
 625 630 635 640  
 Asn Asp Gln Val Met Val Gly Tyr Tyr Val Asn Asp Asn Lys Gln Gly  
 645 650 655  
 Asn Trp Gln Tyr Lys Ser Leu Asp Val Asn Val Asn Ile Glu Gln Asn  
 660 665 670  
 Phe Ile Pro Asp Ile Asp Ser Ala Val Arg Ile Ile Pro Val Asn Tyr  
 675 680 685  
 Asp Ser Asp Pro Lys Leu Asp Ser Gln Leu Tyr Thr Val Glu Met Thr  
 690 695 700

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Ile Pro Ala Gly Val Ser Ala Val Lys Ile Ala Pro Thr Asp Ser Leu  
705 710 715 720

Thr Ser Ser Gly Gln Gln Ile Gly Lys Leu Val Asn Val Asn Asn Pro  
725 730 735

Asp Gln Asn Met Asn Tyr Tyr Ile Arg Lys Asp Ser Gly Ala Gly Asn  
740 745 750

Phe Met Ala Gly Gln Lys Gly Ser Phe Pro Val Lys Glu Asn Thr Ser  
755 760 765

Tyr Thr Phe Ser Ala Ile Tyr Thr Gly Gly Glu Tyr Pro Asn Ser Gly  
770 775 780

Tyr Ser Ser Gly Thr Tyr Ala Gly Asn Leu Thr Val Ser Phe Tyr Ser  
785 790 795 800

Asn Asp Asn Lys Gln Gly Asn Trp Gln Tyr Lys Ser Leu Asp Val Asn  
805 810 815

Val Asn Ile Glu Gln Leu Glu His His His His His His  
820 825

&lt;210&gt; SEQ ID NO 20

&lt;211&gt; LENGTH: 3405

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Escherichia coli

&lt;400&gt; SEQUENCE: 20

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atgaataaaa ttttatttat ttttacattg tttttttctt cagggttttt tacatttgcc      60
gtatcggcag ataaaaatcc cggaagtga aacatgacta atactattgg tccccatgac      120
agggggggat cttcccccat atataatc ttaaattcct atcttacagc atacaatgga      180
agccatcatc tgtatgatag gatgagtttt ttatgtttgt cttctcaaaa tacactgaat      240
ggagcatgcc caagcagtga tgcacctgac actgctacaa ttgatggcga aacaaatata      300
acattacaat ttacggaaaa aagaagtcta attaaaagag aactgcaaat taaaggctat      360
aaacaatttt tgttcaaaaa tgctaattgc ccatcetaaac tagcacttaa ctcatetcat      420
tttcaatgta atagagaaca agcttcaggt gctactttat cgttatacat accagctggt      480
gaattaaata aattaccttt tggggggggtc tggaaatgccg ttctgaagct aaatgtaaaa      540
agacgatatg atacaaccta tgggacttac actataaaca tcacagttaa ttaactgat      600
aagggaataa ttcagatgat gttaccacag ttcaaaagta acgctcgtgt cgatcttaac      660
ttgctgctca ctggtggtgg tacatatatc ggaagaaatt ctgttgatat gtgcttttat      720
gatggatata gtactaacag cagctcttta gagataagat ttcaggatga taattctaaa      780
tctgatggaa aattttatct aaagaaaata aatgatgact ccaaagaact tgtatacact      840
ttgtcacttc tcctggcagg taaaaattta acaccaacaa atggacaggc attaaatatt      900
aacactgctt ctctggaaac aaactggaat agaattacag ctgtcaccat gccagaaatc      960
agtgttccgg tgttgtgttg gctcggacgt ttgcaattgg atgcaaaagt gaaaaatccc     1020
gaggctggac aatatatggg gaatattaaa attactttca caccaagtag tcaaacactc     1080
gacaataaac aagtagagaa aaatattact gtaacagcta gtgttgatcc tgcaattgat     1140
cttttgcaag ctgatggcaa tgctctgcca tcagctgtaa agttagetta ttctcccgca     1200
tcaaaaactt ttgaaagtta cagagtaatg actcaagttc atacaaacga tgcaactaaa     1260
aaagtaattg ttaaacttgc tgatacacca cagcttacag atgttctgaa ttaactggt     1320
caaatgccta tcagtgtgtc atggggagga caagtattat ctacaacagc caaagaattt     1380
gaagctgctg ctttgggata ttctgcatcc ggtgtaaatg gcgtatcatc ttctcaagag     1440

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ttagtaatta gcgctgcacc taaaactgcc ggtaccgccc caactgcagg aaactattca 1500
ggagtagtat ctcttgaat gactttggga tccgacaata aacaagtaga gaaaaatatt 1560
actgtaacag ctagtgtoga cctactatt gatattcttc aagcaaatgg ttctgcgcta 1620
ccgacagctg tagatttaac ttatctacct ggtgcaaaaa cttttgaaaa ttacagtgtt 1680
ctaaccaga tttacacaaa tgacccttca aaaggtttag atgttcgact ggttgataca 1740
ccgaaactta caaatatfff gcaaccgaca tctaccattc ctcttactgt ctcatgggca 1800
gggaagacat taagtacaag tgctcagaag attgcagttg gcgatctggg ttttggttcc 1860
accggaacgg caggtgtttc gaatagtaa gaattagtaa ttggagcaac tacatccgga 1920
actgcaccaa gtgcaggtaa gtatcaaggc gtcgtttcca ttgtaatgac tcaatcgacc 1980
gacacagccg cgctgttcc tgacaataaa caagtagaga aaaatattac tgtgacagcc 2040
agtgttgatc ctactattga cattttgcaa gctgatggta gtagtttacc tactgctgta 2100
gaattaacct attcacctgc ggcaagtcgt tttgaaaatt ataaaatcgc aactaaagt 2160
catacaaatg ttataataa aaatgtacta gttaaagctt taaatgatcc aaaacttaca 2220
aatgttttgg attctacaaa acaactccc attactgtat catatggagg aaagactcta 2280
tcaaccgagc atgtgacttt tgaacctgca gaattaaatt ttggaacgct aggtgtaact 2340
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ggaaattata gtggggtcgt ttctatctta atgaccttag catcagacaa taaacaagt 2460
gaaaaaata tcaactgaac agctagtgtt gatcctacgg gcgagcaaaa ttttattcca 2520
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tcacagttat atacggttga gatgacgatc cctgcaggtg taagcgcagt taaaatcgta 2640
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actggtggcg aataccctaa tagcggatat tegtctgcta cttatgcagg acatttgact 2880
gtatcatttt acagcaatga caataaacia agaacagaaa tagcggactaa aaacttccca 2940
gtatcaacga ctatttcaaa aagttttttt gcgcctgaac cacaatcca gccttctttt 3000
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gtaaataccg ctgatgatc ccaatcaata atctaccaga ttgttgatga taaagggaaa 3180
aaaatgtaa aagatcatgg tacagagggt acgcctaate aacaaataac ttttaaagcg 3240
ctgaattata ctagcggaga taaagaata cctcctggga tatataacga tcaggttatg 3300
gttggttact acgtaaacga caataaacia ggaactggc aatataaatc tctggatgta 3360
aatgtaaata ttgagcaact cgagcaccac caccaccacc actga 3405

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&lt;210&gt; SEQ ID NO 21

&lt;211&gt; LENGTH: 1134

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Escherichia coli

&lt;400&gt; SEQUENCE: 21

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Met Asn Lys Ile Leu Phe Ile Phe Thr Leu Phe Phe Ser Ser Gly Phe
1           5           10          15

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Phe Thr Phe Ala Val Ser Ala Asp Lys Asn Pro Gly Ser Glu Asn Met

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20					25					30					
Thr	Asn	Thr	Ile	Gly	Pro	His	Asp	Arg	Gly	Gly	Ser	Ser	Pro	Ile	Tyr
	35						40					45			
Asn	Ile	Leu	Asn	Ser	Tyr	Leu	Thr	Ala	Tyr	Asn	Gly	Ser	His	His	Leu
	50					55					60				
Tyr	Asp	Arg	Met	Ser	Phe	Leu	Cys	Leu	Ser	Ser	Gln	Asn	Thr	Leu	Asn
65					70					75					80
Gly	Ala	Cys	Pro	Ser	Ser	Asp	Ala	Pro	Gly	Thr	Ala	Thr	Ile	Asp	Gly
				85					90					95	
Glu	Thr	Asn	Ile	Thr	Leu	Gln	Phe	Thr	Glu	Lys	Arg	Ser	Leu	Ile	Lys
		100						105					110		
Arg	Glu	Leu	Gln	Ile	Lys	Gly	Tyr	Lys	Gln	Phe	Leu	Phe	Lys	Asn	Ala
	115						120					125			
Asn	Cys	Pro	Ser	Lys	Leu	Ala	Leu	Asn	Ser	Ser	His	Phe	Gln	Cys	Asn
	130					135					140				
Arg	Glu	Gln	Ala	Ser	Gly	Ala	Thr	Leu	Ser	Leu	Tyr	Ile	Pro	Ala	Gly
145					150					155					160
Glu	Leu	Asn	Lys	Leu	Pro	Phe	Gly	Gly	Val	Trp	Asn	Ala	Val	Leu	Lys
			165						170						175
Leu	Asn	Val	Lys	Arg	Arg	Tyr	Asp	Thr	Thr	Tyr	Gly	Thr	Tyr	Thr	Ile
		180						185						190	
Asn	Ile	Thr	Val	Asn	Leu	Thr	Asp	Lys	Gly	Asn	Ile	Gln	Ile	Trp	Leu
	195						200					205			
Pro	Gln	Phe	Lys	Ser	Asn	Ala	Arg	Val	Asp	Leu	Asn	Leu	Arg	Pro	Thr
	210					215					220				
Gly	Gly	Gly	Thr	Tyr	Ile	Gly	Arg	Asn	Ser	Val	Asp	Met	Cys	Phe	Tyr
225					230					235					240
Asp	Gly	Tyr	Ser	Thr	Asn	Ser	Ser	Ser	Ser	Leu	Glu	Ile	Arg	Phe	Gln
			245							250					255
Asp	Asn	Ser	Lys	Ser	Asp	Gly	Lys	Phe	Tyr	Leu	Lys	Lys	Ile	Asn	Asp
		260						265						270	
Asp	Ser	Lys	Glu	Leu	Val	Tyr	Thr	Leu	Ser	Leu	Leu	Leu	Ala	Gly	Lys
		275					280						285		
Asn	Leu	Thr	Pro	Thr	Asn	Gly	Gln	Ala	Leu	Asn	Ile	Asn	Thr	Ala	Ser
	290					295					300				
Leu	Glu	Thr	Asn	Trp	Asn	Arg	Ile	Thr	Ala	Val	Thr	Met	Pro	Glu	Ile
305					310					315					320
Ser	Val	Pro	Val	Leu	Cys	Trp	Pro	Gly	Arg	Leu	Gln	Leu	Asp	Ala	Lys
				325					330						335
Val	Lys	Asn	Pro	Glu	Ala	Gly	Gln	Tyr	Met	Gly	Asn	Ile	Lys	Ile	Thr
		340						345						350	
Phe	Thr	Pro	Ser	Ser	Gln	Thr	Leu	Asp	Asn	Lys	Gln	Val	Glu	Lys	Asn
		355					360						365		
Ile	Thr	Val	Thr	Ala	Ser	Val	Asp	Pro	Ala	Ile	Asp	Leu	Leu	Gln	Ala
	370					375					380				
Asp	Gly	Asn	Ala	Leu	Pro	Ser	Ala	Val	Lys	Leu	Ala	Tyr	Ser	Pro	Ala
385					390					395					400
Ser	Lys	Thr	Phe	Glu	Ser	Tyr	Arg	Val	Met	Thr	Gln	Val	His	Thr	Asn
			405						410						415
Asp	Ala	Thr	Lys	Lys	Val	Ile	Val	Lys	Leu	Ala	Asp	Thr	Pro	Gln	Leu
			420						425					430	
Thr	Asp	Val	Leu	Asn	Ser	Thr	Val	Gln	Met	Pro	Ile	Ser	Val	Ser	Trp
		435						440						445	

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Gly Gly Gln Val Leu Ser Thr Thr Ala Lys Glu Phe Glu Ala Ala Ala  
 450 455 460  
 Leu Gly Tyr Ser Ala Ser Gly Val Asn Gly Val Ser Ser Ser Gln Glu  
 465 470 475 480  
 Leu Val Ile Ser Ala Ala Pro Lys Thr Ala Gly Thr Ala Pro Thr Ala  
 485 490 495  
 Gly Asn Tyr Ser Gly Val Val Ser Leu Val Met Thr Leu Gly Ser Asp  
 500 505 510  
 Asn Lys Gln Val Glu Lys Asn Ile Thr Val Thr Ala Ser Val Asp Pro  
 515 520 525  
 Thr Ile Asp Ile Leu Gln Ala Asn Gly Ser Ala Leu Pro Thr Ala Val  
 530 535 540  
 Asp Leu Thr Tyr Leu Pro Gly Ala Lys Thr Phe Glu Asn Tyr Ser Val  
 545 550 555 560  
 Leu Thr Gln Ile Tyr Thr Asn Asp Pro Ser Lys Gly Leu Asp Val Arg  
 565 570 575  
 Leu Val Asp Thr Pro Lys Leu Thr Asn Ile Leu Gln Pro Thr Ser Thr  
 580 585 590  
 Ile Pro Leu Thr Val Ser Trp Ala Gly Lys Thr Leu Ser Thr Ser Ala  
 595 600 605  
 Gln Lys Ile Ala Val Gly Asp Leu Gly Phe Gly Ser Thr Gly Thr Ala  
 610 615 620  
 Gly Val Ser Asn Ser Lys Glu Leu Val Ile Gly Ala Thr Thr Ser Gly  
 625 630 635 640  
 Thr Ala Pro Ser Ala Gly Lys Tyr Gln Gly Val Val Ser Ile Val Met  
 645 650 655  
 Thr Gln Ser Thr Asp Thr Ala Ala Pro Val Pro Asp Asn Lys Gln Val  
 660 665 670  
 Glu Lys Asn Ile Thr Val Thr Ala Ser Val Asp Pro Thr Ile Asp Ile  
 675 680 685  
 Leu Gln Ala Asp Gly Ser Ser Leu Pro Thr Ala Val Glu Leu Thr Tyr  
 690 695 700  
 Ser Pro Ala Ala Ser Arg Phe Glu Asn Tyr Lys Ile Ala Thr Lys Val  
 705 710 715 720  
 His Thr Asn Val Ile Asn Lys Asn Val Leu Val Lys Leu Val Asn Asp  
 725 730 735  
 Pro Lys Leu Thr Asn Val Leu Asp Ser Thr Lys Gln Leu Pro Ile Thr  
 740 745 750  
 Val Ser Tyr Gly Gly Lys Thr Leu Ser Thr Ala Asp Val Thr Phe Glu  
 755 760 765  
 Pro Ala Glu Leu Asn Phe Gly Thr Ser Gly Val Thr Gly Val Ser Ser  
 770 775 780  
 Ser Gln Asp Leu Val Ile Gly Ala Thr Thr Ala Gln Ala Pro Thr Ala  
 785 790 795 800  
 Gly Asn Tyr Ser Gly Val Val Ser Ile Leu Met Thr Leu Ala Ser Asp  
 805 810 815  
 Asn Lys Gln Val Glu Lys Asn Ile Thr Val Thr Ala Ser Val Asp Pro  
 820 825 830  
 Thr Gly Glu Gln Asn Phe Ile Pro Asp Ile Asp Ser Ala Val Arg Ile  
 835 840 845  
 Ile Pro Val Asn Tyr Asp Ser Asp Pro Lys Leu Asn Ser Gln Leu Tyr  
 850 855 860

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Thr Val Glu Met Thr Ile Pro Ala Gly Val Ser Ala Val Lys Ile Val  
 865 870 875 880

Pro Thr Asp Ser Leu Thr Ser Ser Gly Gln Gln Ile Gly Lys Leu Val  
 885 890 895

Asn Val Asn Asn Pro Asp Gln Asn Met Asn Tyr Tyr Ile Arg Lys Asp  
 900 905 910

Ser Gly Ala Gly Lys Phe Met Ala Gly Gln Lys Gly Ser Phe Ser Val  
 915 920 925

Lys Glu Asn Thr Ser Tyr Thr Phe Ser Ala Ile Tyr Thr Gly Gly Glu  
 930 935 940

Tyr Pro Asn Ser Gly Tyr Ser Ser Gly Thr Tyr Ala Gly His Leu Thr  
 945 950 955 960

Val Ser Phe Tyr Ser Asn Asp Asn Lys Gln Arg Thr Glu Ile Ala Thr  
 965 970 975

Lys Asn Phe Pro Val Ser Thr Thr Ile Ser Lys Ser Phe Phe Ala Pro  
 980 985 990

Glu Pro Gln Ile Gln Pro Ser Phe Gly Lys Asn Val Gly Lys Glu Gly  
 995 1000 1005

Asp Leu Leu Phe Ser Val Ser Leu Ile Val Pro Glu Asn Val Ser  
 1010 1015 1020

Gln Val Thr Val Tyr Pro Val Tyr Asp Glu Asp Tyr Gly Leu Gly  
 1025 1030 1035

Arg Leu Val Asn Thr Ala Asp Asp Ser Gln Ser Ile Ile Tyr Gln  
 1040 1045 1050

Ile Val Asp Asp Lys Gly Lys Lys Met Leu Lys Asp His Gly Thr  
 1055 1060 1065

Glu Val Thr Pro Asn Gln Gln Ile Thr Phe Lys Ala Leu Asn Tyr  
 1070 1075 1080

Thr Ser Gly Asp Lys Glu Ile Pro Pro Gly Ile Tyr Asn Asp Gln  
 1085 1090 1095

Val Met Val Gly Tyr Tyr Val Asn Asp Asn Lys Gln Gly Asn Trp  
 1100 1105 1110

Gln Tyr Lys Ser Leu Asp Val Asn Val Asn Ile Glu Gln Leu Glu  
 1115 1120 1125

His His His His His His  
 1130

<210> SEQ ID NO 22  
 <211> LENGTH: 3342  
 <212> TYPE: DNA  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 22

atggcagata aaaatcccgg aagtgaaaac atgactaata ctattggtcc ccatgacagg 60

gggggatctt ccccatata taatatctta aattcctatc ttacagcata caatggaagc 120

catcatctgt atgataggat gagtttttta tgtttgtctt ctcaaaatac actgaatgga 180

gcatgcccaa gcagtgatgc ccttggaact gctacaattg atggcgaaac aaatataaca 240

ttacaattta cggaaaaaag aagtctaatt aaaagagaac tgcaaatata aggctataaa 300

caatttttgt tcaaaaatgc taattgcca tctaaactag cacttaactc atctcatttt 360

caatgtaata gagaacaagc ttcaggtgct actttatcgt tatacatacc agctggtgaa 420

ttaaataaat taccttttgg gggggtctgg aatgccgttc tgaagctaaa tgtaaaaaga 480

cgatatgata caacctatgg gacttacact ataaacatca cagttaattt aactgataag 540

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ggaaatattc agatatgggtt accacagttc aaaagtaacg ctctgttoga tcttaacttg	600
cgtccaactg gtgggtgttac atatatcgga agaaattctg ttgatatgtg cttttatgat	660
ggatatagta ctaacagcag ctcttttagag ataagatttc aggatgataa ttctaaatct	720
gatggaaaat tttatctaaa gaaaataaat gatgactcca aagaacttgt atacactttg	780
tcacttctcc tggcaggtaa aaatttaaca ccaacaaatg gacaggcatt aatatattaac	840
actgcttctc tggaaacaaa ctggaataga attacagctg tcaccatgcc agaaatcagt	900
gttccggtgt tgtgttggcc tggacgtttg caattggatg caaaagtga aaatcccag	960
gctggacaat atatggggaa tattaaaatt actttcacac caagtagtca aacactcgac	1020
aataaacaag tagagaaaaa tattactgta acagctagtg ttgatccctg aattgatcct	1080
ttgcaagctg atggcaatgc tctgccatca gctgtaaagt tagcttattc tcccgcata	1140
aaaacttttg aaagttacag agtaatgact caagttcata caaacgatgc aactaaaaa	1200
gtaattgtta aacttgctga tacaccacag cttacagatg ttctgaattc aactgttcaa	1260
atgcctatca gtgtgtcatg gggaggacaa gtattatcta caacagccaa agaatttgaa	1320
gctgctgctt tgggatattc tgcacccggt gtaaatggcg tatcatcttc tcaagagtta	1380
gtaattagcg ctgcacctaa aactgcccgt accgcccaca ctgcaggaaa ctattcagga	1440
gtagtatctc ttgtaatgac tttgggatcc gacaataaac aagtagagaa aaatattact	1500
gtaacagcta gtgtcgacc tactattgat attcttcaag caaatggttc tgcgctaccg	1560
acagctgtag atttaactta tctacctggt gcaaaaactt ttgaaaatta cagtgttcta	1620
accagattt acacaaaatga ccttcaaaa ggtttagatg ttcgactggt tgatacaccg	1680
aaacttacaa atattttgca accgacatct accattcctc ttactgtctc atgggcaggg	1740
aagacattaa gtacaagtgc tcagaagatt gcagttggcg atctgggttt tggttccacc	1800
ggaaacggcag gtgtttcgaa tagtaagaa ttagtaattg gagcaactac atccggaact	1860
gcaccaagtg caggtaaagta tcaaggcgtc gtttccattg taatgactca atcgaccgac	1920
acagccgcgc ctgttctcga caataaaca gttagaaaaa atattactgt gacagccagt	1980
gttgatccta ctattgacat tttgcaagct gatggtagta gtttacctac tgetgtagaa	2040
ttaacctatt cacctgcccg aagtcgtttt gaaaattata aaatcgcaac taaagttcat	2100
acaaatgtta taaataaaaa tgtactagtt aagcttgtaa atgatccaaa acttacaaat	2160
gttttgatt ctacaaaaa actcccatt actgtatcat atggaggaaa gactctatca	2220
accgcagatg tgacttttga acctgcagaa ttaaattttg gaacgtcagg tgtaactggt	2280
gtatcttctt cccaagattt agtgattggt gcgactacag cacaagcacc aacggcggga	2340
aattatagtg gggctgtttc tatcttaatg accttagcat cagacaataa acaagtggaa	2400
aaaaatatca ctgtaacagc tagtgttgat cctacggcgc agcaaaattt tattccagat	2460
attgattccg ctgttcgtat aatacctgtt aattacgatt cggatccgaa actgaattca	2520
cagttatata cggttgagat gacgatccct gcaggtgtaa gcgcagttaa aatcgtacca	2580
acagatagtc tgacatcttc tggacagcag atcggaaaagc tggttaatgt aaacaatcca	2640
gatcaaaata tgaattatta tatcagaaag gattctggcg ctggttaagt tatggcaggg	2700
caaaaaggat ccttttctgt caaagagaat acgtcataka cattctcagc aatttatact	2760
ggtggcgaat accctaatag cggatattcg tctggtactt atgcaggaca tttgactgta	2820
tcattttaca gcaatgacaa taaacaaaga acagaaatag cgactaaaaa cttcccagta	2880

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tcaacgacta tttcaaaaag tttttttgcg cctgaaccac aaatccagcc ttcttttgg 2940
aaaaatgttg gaaaggaagg agatttatta ttagtggtga gcttaattgt tcctgaaat 3000
gtatcccagg taacggctca cctgtttat gatgaagatt atggattagg acgactcgta 3060
aataccgctg atgattccca atcaataatc taccagattg ttgatgataa agggaaaaaa 3120
atgttaaaag atcatggtag agaggttacg cctaatacaac aaataacttt taaagcgctg 3180
aattatacta gcggagataa agaatacct cctgggatat ataacgatca ggttatggtt 3240
ggttactacg taaacgacaa taaacaagga aactggcaat ataaatctct ggatgtaaat 3300
gtaaatttg agcaactoga gcaccaccac caccaccact ga 3342

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&lt;210&gt; SEQ ID NO 23

&lt;211&gt; LENGTH: 1113

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Escherichia coli

&lt;400&gt; SEQUENCE: 23

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Met Ala Asp Lys Asn Pro Gly Ser Glu Asn Met Thr Asn Thr Ile Gly
1           5           10          15
Pro His Asp Arg Gly Gly Ser Ser Pro Ile Tyr Asn Ile Leu Asn Ser
20          25          30
Tyr Leu Thr Ala Tyr Asn Gly Ser His His Leu Tyr Asp Arg Met Ser
35          40          45
Phe Leu Cys Leu Ser Ser Gln Asn Thr Leu Asn Gly Ala Cys Pro Ser
50          55          60
Ser Asp Ala Pro Gly Thr Ala Thr Ile Asp Gly Glu Thr Asn Ile Thr
65          70          75          80
Leu Gln Phe Thr Glu Lys Arg Ser Leu Ile Lys Arg Glu Leu Gln Ile
85          90          95
Lys Gly Tyr Lys Gln Phe Leu Phe Lys Asn Ala Asn Cys Pro Ser Lys
100         105         110
Leu Ala Leu Asn Ser Ser His Phe Gln Cys Asn Arg Glu Gln Ala Ser
115         120         125
Gly Ala Thr Leu Ser Leu Tyr Ile Pro Ala Gly Glu Leu Asn Lys Leu
130         135         140
Pro Phe Gly Gly Val Trp Asn Ala Val Leu Lys Leu Asn Val Lys Arg
145         150         155         160
Arg Tyr Asp Thr Thr Tyr Gly Thr Tyr Thr Ile Asn Ile Thr Val Asn
165         170         175
Leu Thr Asp Lys Gly Asn Ile Gln Ile Trp Leu Pro Gln Phe Lys Ser
180         185         190
Asn Ala Arg Val Asp Leu Asn Leu Arg Pro Thr Gly Gly Gly Thr Tyr
195         200         205
Ile Gly Arg Asn Ser Val Asp Met Cys Phe Tyr Asp Gly Tyr Ser Thr
210         215         220
Asn Ser Ser Ser Leu Glu Ile Arg Phe Gln Asp Asp Asn Ser Lys Ser
225         230         235         240
Asp Gly Lys Phe Tyr Leu Lys Lys Ile Asn Asp Asp Ser Lys Glu Leu
245         250         255
Val Tyr Thr Leu Ser Leu Leu Leu Ala Gly Lys Asn Leu Thr Pro Thr
260         265         270
Asn Gly Gln Ala Leu Asn Ile Asn Thr Ala Ser Leu Glu Thr Asn Trp
275         280         285
Asn Arg Ile Thr Ala Val Thr Met Pro Glu Ile Ser Val Pro Val Leu

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290					295					300					
Cys	Trp	Pro	Gly	Arg	Leu	Gln	Leu	Asp	Ala	Lys	Val	Lys	Asn	Pro	Glu
305					310					315					320
Ala	Gly	Gln	Tyr	Met	Gly	Asn	Ile	Lys	Ile	Thr	Phe	Thr	Pro	Ser	Ser
				325					330					335	
Gln	Thr	Leu	Asp	Asn	Lys	Gln	Val	Glu	Lys	Asn	Ile	Thr	Val	Thr	Ala
			340					345					350		
Ser	Val	Asp	Pro	Ala	Ile	Asp	Leu	Leu	Gln	Ala	Asp	Gly	Asn	Ala	Leu
		355					360					365			
Pro	Ser	Ala	Val	Lys	Leu	Ala	Tyr	Ser	Pro	Ala	Ser	Lys	Thr	Phe	Glu
		370				375					380				
Ser	Tyr	Arg	Val	Met	Thr	Gln	Val	His	Thr	Asn	Asp	Ala	Thr	Lys	Lys
385				390						395					400
Val	Ile	Val	Lys	Leu	Ala	Asp	Thr	Pro	Gln	Leu	Thr	Asp	Val	Leu	Asn
				405					410					415	
Ser	Thr	Val	Gln	Met	Pro	Ile	Ser	Val	Ser	Trp	Gly	Gly	Gln	Val	Leu
			420					425					430		
Ser	Thr	Thr	Ala	Lys	Glu	Phe	Glu	Ala	Ala	Ala	Leu	Gly	Tyr	Ser	Ala
			435				440					445			
Ser	Gly	Val	Asn	Gly	Val	Ser	Ser	Ser	Gln	Glu	Leu	Val	Ile	Ser	Ala
	450				455					460					
Ala	Pro	Lys	Thr	Ala	Gly	Thr	Ala	Pro	Thr	Ala	Gly	Asn	Tyr	Ser	Gly
465				470					475						480
Val	Val	Ser	Leu	Val	Met	Thr	Leu	Gly	Ser	Asp	Asn	Lys	Gln	Val	Glu
				485					490					495	
Lys	Asn	Ile	Thr	Val	Thr	Ala	Ser	Val	Asp	Pro	Thr	Ile	Asp	Ile	Leu
			500					505					510		
Gln	Ala	Asn	Gly	Ser	Ala	Leu	Pro	Thr	Ala	Val	Asp	Leu	Thr	Tyr	Leu
		515					520					525			
Pro	Gly	Ala	Lys	Thr	Phe	Glu	Asn	Tyr	Ser	Val	Leu	Thr	Gln	Ile	Tyr
	530				535					540					
Thr	Asn	Asp	Pro	Ser	Lys	Gly	Leu	Asp	Val	Arg	Leu	Val	Asp	Thr	Pro
545				550					555					560	
Lys	Leu	Thr	Asn	Ile	Leu	Gln	Pro	Thr	Ser	Thr	Ile	Pro	Leu	Thr	Val
			565					570					575		
Ser	Trp	Ala	Gly	Lys	Thr	Leu	Ser	Thr	Ser	Ala	Gln	Lys	Ile	Ala	Val
		580						585					590		
Gly	Asp	Leu	Gly	Phe	Gly	Ser	Thr	Gly	Thr	Ala	Gly	Val	Ser	Asn	Ser
	595					600					605				
Lys	Glu	Leu	Val	Ile	Gly	Ala	Thr	Thr	Ser	Gly	Thr	Ala	Pro	Ser	Ala
	610				615					620					
Gly	Lys	Tyr	Gln	Gly	Val	Val	Ser	Ile	Val	Met	Thr	Gln	Ser	Thr	Asp
625				630						635					640
Thr	Ala	Ala	Pro	Val	Pro	Asp	Asn	Lys	Gln	Val	Glu	Lys	Asn	Ile	Thr
			645						650					655	
Val	Thr	Ala	Ser	Val	Asp	Pro	Thr	Ile	Asp	Ile	Leu	Gln	Ala	Asp	Gly
			660					665					670		
Ser	Ser	Leu	Pro	Thr	Ala	Val	Glu	Leu	Thr	Tyr	Ser	Pro	Ala	Ala	Ser
		675					680					685			
Arg	Phe	Glu	Asn	Tyr	Lys	Ile	Ala	Thr	Lys	Val	His	Thr	Asn	Val	Ile
	690					695					700				
Asn	Lys	Asn	Val	Leu	Val	Lys	Leu	Val	Asn	Asp	Pro	Lys	Leu	Thr	Asn
705				710						715				720	



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&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Escherichia coli

&lt;400&gt; SEQUENCE: 24

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atgaaaaaga tatttatttt tttgtctatc atattttctg cggtggtcag tgccgggcca      60
taccgggaaa ctacagtagg taatctgacg aagagttttc aagcccctcg tcaggataga      120
agcgtacaat caccaatata taacatcttt acgaatcatg tggctggata tagtttgagt      180
cataacttat atgacaggat tgttttttta tgtacatcct cgtcgaatcc ggttaatggt      240
gcttgcccaa ccattggaac atctggagtt caatacggta ctacaacccat aaccttgca      300
tttacagaaa aaagaagtct gataaaaaga aatattaatc ttgcaggtaa taagaaacca      360
atatgggaga atcagagttg cgacactagc aatctaattg tghtgaattc gaagtcttgg      420
tccttggggg cttacggaaa tgtaacgga acacttctaa atctgtatat cctgcagga      480
gaaatcaaca aattgccttt tggagggata tgggaggcaa ctctgatctt acgcttatca      540
agatatggcg aagtcagtag cacccattac ggcaattata ccgtaaatat tacggttgat      600
ttaactgata aagtaatat tcaggatagg cttccagggt ttcacagcaa cccgcgtgta      660
gacctgaatc tgcaccctat cgtaattat aaatatagtg gtagtaattc actcgacatg      720
tgtttctatg atggatatag tacaaacagt gatagcatgg taataaagt ccaggatgat      780
aatcctacct attcatctga atataatctt tataagatag ggggcaactga aaaattacce      840
tatgctgttt cactgcttat gggagaaaaa atattttatc cagtgaatgg tcaatcattt      900
actatcaatg acagtagtgt actcgaaca aactggaatc gagtaaccgc agttgctatg      960
ccggaagtta atgttccagt attatgctgg ccagcaagat tgctattaaa tgctgatgta     1020
aatgctcccg atgcaggaca gtattcagga cagatatata taacatttac acccagtgtc     1080
gaaaatttag gcggtggagt cgaaaaaat attactgtga gggcaagtgt tgaccctaaa     1140
cttgatcttc tgcaagcaga tggaaactca ctgccggact ctatcgatt aacctattct     1200
tcggcttcaa ataatttga agtttactct ctttaactg ctattcatac aaatgacaaa     1260
agcaagggag ttgtagttaa gctgtcagct tcaccagttc tgtccaatat tatgaagcca     1320
aactcgcaaa ttccgatgaa agtgactttg ggggggaaga cgctgaatac aactgatact     1380
gagtttactg ttgatactct gaactttggt acatctggtg ttgaaaactg ttcttccact     1440
caacagctta cgattcatgc agacacacaa ggaactgcgc ctgaggcagg caattaccaa     1500
ggattatttt ctcttatcat gactcaaaaa acagggggcg gtgtcgaaaa aaatattact     1560
gtgagggcaa gtgtcgacc taaactgac cttctgcaat ctgatggctc tgcgctgccg     1620
aactctgtcg cattaacctt ttctccggct gtaaataatt ttgaagctca caccatcaac     1680
accgtgttcc atacaaatga ctacagataa ggtgttgttg tgaagctgtc agcagatcca     1740
gtcctgtcca atgttctgaa tccaaccctg caaattcctg tttctgtgaa tttcgcagga     1800
aaaccactga gcacaacagg cattaccatc gactccaatg atctgaactt tgcttcgagt     1860
ggtgttaata aagtttcttc tacgcagaaa ctttcaatcc atgcagatgc tactcgggta     1920
actggcggcg cactaacagc tggtaaatat cagggactcg tatcaattat cctgactaag     1980
tcaacggggg gcggtgtcga gaagaccatt agcgttacgg cgagtgttga cccgacgggc     2040
gagcaaaatt ttattccaga tattgattcc gctgttcgta taatacctgt taattacgat     2100
tcggatccga aactgaattc acagttatat acggttgaga tgacgatccc tgcaggtgta     2160
agcgcagtta aaatcgtacc aacagatagt ctgacatctt ctggacagca gatcggaaaag     2220

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ctggttaatg taaacaatcc agatcaaaat atgaattatt atatcagaaa ggattctggc 2280
gctggtaagt ttatggcagg gcaaaaagga tccttttctg tcaaagagaa tacgtcatac 2340
acattctcag caatttatac tggtagcgaa taccctaata gcggatattc gtctggtact 2400
tatgcaggac atttgactgt atcattttac agcaatgaca ataaacaaag aacagaaata 2460
gcgactaaaa acttcccagt atcaacgact atttcaaaaa gtttttttgc gcctgaacca 2520
caaatccagc cttcttttgg taaaaatgtt ggaaaggaag gagatttatt atttagtgtg 2580
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tatggattag gacgactcgt aaataccgct gatgattccc aatcaataat ctaccagatt 2700
gttgatgata aagggaaaaa aatggttaaaa gatcatggta cagaggttac gcctaatcaa 2760
caaataactt ttaaagcgct gaattatact agcggagata aagaatacc tcctgggata 2820
tataacgatac aggttatggg tggttactac gtaaacgaca ataaacaagg aaactggcaa 2880
tataaatctc tggatgtaaa tgtaaatatt gagcaactcg agcaccacca ccaccaccac 2940
tga 2943

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&lt;210&gt; SEQ ID NO 25

&lt;211&gt; LENGTH: 980

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Escherichia coli

&lt;400&gt; SEQUENCE: 25

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Met Lys Lys Ile Phe Ile Phe Leu Ser Ile Ile Phe Ser Ala Val Val
 1          5          10          15
Ser Ala Gly Arg Tyr Pro Glu Thr Thr Val Gly Asn Leu Thr Lys Ser
 20          25          30
Phe Gln Ala Pro Arg Gln Asp Arg Ser Val Gln Ser Pro Ile Tyr Asn
 35          40          45
Ile Phe Thr Asn His Val Ala Gly Tyr Ser Leu Ser His Asn Leu Tyr
 50          55          60
Asp Arg Ile Val Phe Leu Cys Thr Ser Ser Ser Asn Pro Val Asn Gly
 65          70          75          80
Ala Cys Pro Thr Ile Gly Thr Ser Gly Val Gln Tyr Gly Thr Thr Thr
 85          90          95
Ile Thr Leu Gln Phe Thr Glu Lys Arg Ser Leu Ile Lys Arg Asn Ile
 100         105         110
Asn Leu Ala Gly Asn Lys Lys Pro Ile Trp Glu Asn Gln Ser Cys Asp
 115         120         125
Thr Ser Asn Leu Met Val Leu Asn Ser Lys Ser Trp Ser Cys Gly Ala
 130         135         140
Tyr Gly Asn Ala Asn Gly Thr Leu Leu Asn Leu Tyr Ile Pro Ala Gly
 145         150         155         160
Glu Ile Asn Lys Leu Pro Phe Gly Gly Ile Trp Glu Ala Thr Leu Ile
 165         170         175
Leu Arg Leu Ser Arg Tyr Gly Glu Val Ser Ser Thr His Tyr Gly Asn
 180         185         190
Tyr Thr Val Asn Ile Thr Val Asp Leu Thr Asp Lys Gly Asn Ile Gln
 195         200         205
Val Trp Leu Pro Gly Phe His Ser Asn Pro Arg Val Asp Leu Asn Leu
 210         215         220
His Pro Ile Gly Asn Tyr Lys Tyr Ser Gly Ser Asn Ser Leu Asp Met
 225         230         235         240

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660					665					670					
Thr	Ala	Ser	Val	Asp	Pro	Thr	Gly	Glu	Gln	Asn	Phe	Ile	Pro	Asp	Ile
	675						680					685			
Asp	Ser	Ala	Val	Arg	Ile	Ile	Pro	Val	Asn	Tyr	Asp	Ser	Asp	Pro	Lys
	690					695					700				
Leu	Asn	Ser	Gln	Leu	Tyr	Thr	Val	Glu	Met	Thr	Ile	Pro	Ala	Gly	Val
	705					710					715				720
Ser	Ala	Val	Lys	Ile	Val	Pro	Thr	Asp	Ser	Leu	Thr	Ser	Ser	Gly	Gln
			725						730					735	
Gln	Ile	Gly	Lys	Leu	Val	Asn	Val	Asn	Asn	Pro	Asp	Gln	Asn	Met	Asn
			740					745					750		
Tyr	Tyr	Ile	Arg	Lys	Asp	Ser	Gly	Ala	Gly	Lys	Phe	Met	Ala	Gly	Gln
		755					760					765			
Lys	Gly	Ser	Phe	Ser	Val	Lys	Glu	Asn	Thr	Ser	Tyr	Thr	Phe	Ser	Ala
	770					775					780				
Ile	Tyr	Thr	Gly	Gly	Glu	Tyr	Pro	Asn	Ser	Gly	Tyr	Ser	Ser	Gly	Thr
	785					790					795				800
Tyr	Ala	Gly	His	Leu	Thr	Val	Ser	Phe	Tyr	Ser	Asn	Asp	Asn	Lys	Gln
			805						810					815	
Arg	Thr	Glu	Ile	Ala	Thr	Lys	Asn	Phe	Pro	Val	Ser	Thr	Thr	Ile	Ser
			820					825						830	
Lys	Ser	Phe	Phe	Ala	Pro	Glu	Pro	Gln	Ile	Gln	Pro	Ser	Phe	Gly	Lys
		835					840					845			
Asn	Val	Gly	Lys	Glu	Gly	Asp	Leu	Leu	Phe	Ser	Val	Ser	Leu	Ile	Val
	850					855					860				
Pro	Glu	Asn	Val	Ser	Gln	Val	Thr	Val	Tyr	Pro	Val	Tyr	Asp	Glu	Asp
	865					870					875				880
Tyr	Gly	Leu	Gly	Arg	Leu	Val	Asn	Thr	Ala	Asp	Asp	Ser	Gln	Ser	Ile
				885					890					895	
Ile	Tyr	Gln	Ile	Val	Asp	Asp	Lys	Gly	Lys	Lys	Met	Leu	Lys	Asp	His
		900						905					910		
Gly	Thr	Glu	Val	Thr	Pro	Asn	Gln	Gln	Ile	Thr	Phe	Lys	Ala	Leu	Asn
		915						920					925		
Tyr	Thr	Ser	Gly	Asp	Lys	Glu	Ile	Pro	Pro	Gly	Ile	Tyr	Asn	Asp	Gln
	930					935					940				
Val	Met	Val	Gly	Tyr	Tyr	Val	Asn	Asp	Asn	Lys	Gln	Gly	Asn	Trp	Gln
	945					950					955				960
Tyr	Lys	Ser	Leu	Asp	Val	Asn	Val	Asn	Ile	Glu	Gln	Leu	Glu	His	His
				965					970					975	
His	His	His	His												
			980												

<210> SEQ ID NO 26  
 <211> LENGTH: 2795  
 <212> TYPE: DNA  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 26

ttacgaatca tgtggctgga tatagtttga gtcataactt atatgacagg attgtttttt	60
tatgtacatc ctcgtcgaat ceggttaatg gtgcttgecc aaccattgga acatctggag	120
ttcaatacgg tactacaacc ataaccttgc agtttacaga aaaaagaagt ctgataaaaa	180
gaaatattaa tcttgcaggt aataagaaac caatatggga gaatcagagt tgcgacacta	240
gcaatcfaat ggtgttgaat tcgaagtctt ggtcctgtgg ggcttacgga aatgctaacy	300

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gaacacttct	aaatctgtat	atccctgcag	gagaaatcaa	caaattgcct	tttggagga	360
tatgggagge	aactctgac	ttacgcttat	caagatatgg	cgaagtcagt	agcaccatt	420
acggcaatta	taccgtaaat	attacggttg	atttaactga	taaagtaat	attcaggtat	480
ggcttccagg	gtttcacagc	aacccgcgtg	tagacctgaa	tctgcacct	atcgtaatt	540
ataaatatag	tggtagtaat	tcactcgaca	tgtgtttcta	tgatggatat	agtacaaaca	600
gtgatagcat	ggtaataaag	ttccaggatg	ataatcctac	ctattcatct	gaatataatc	660
tttataagat	agggggcact	gaaaaattac	cctatgctgt	ttcactgctt	atgggagaaa	720
aaatatatta	tccagtgaat	ggccaatcat	ttactatcaa	tgacagtagt	gtactcgaaa	780
caaaactggaa	tcgagtaacc	gcagttgcta	tgccggaagt	taatgttcca	gtattatgct	840
ggccagcaag	attgctatta	aatgctgatg	taaatgctcc	cgatgcagga	cagtattcag	900
gacagatata	tataacatth	acaccagtg	tcgaaaatth	agggcgtgga	gtcgaaaaaa	960
atattactgt	gagggcaagt	gttgacccta	aacttgatct	tctgcaagca	gatggaactt	1020
cactgccgga	ctctatcgca	ttaacctatt	cttcggcttc	aaataattht	gaagtttact	1080
ctcttaatac	tgctattcat	acaaatgaca	aaagcaaggg	agttgtagtg	aagctgtcag	1140
cttcaccagt	tctgtccaat	attatgaagc	caaactcgca	aattccgatg	aaagtgactt	1200
tgggggggaa	gacgctgaat	acaactgata	ctgagtttac	tgttgatact	ctgaactttg	1260
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aaacaggggg	cggtgctgaa	aaaaatatta	ctgtgagggc	aagtgtcgac	cctaaaactg	1440
accttctgca	atctgatggc	tctgcgctgc	cgaactctgt	cgcatthaac	tattctccgg	1500
ctgtaaataa	ttttgaagct	cacaccatca	acaccgttgt	tcatacaaat	gactcagata	1560
aaggtgttgt	tgtgaagctg	tcagcagac	cagtctctgc	caatgttctg	aatccaacc	1620
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tcgactccaa	tgatctgaac	tttgcctcga	gtggtgtaa	taaagttctt	tctacgcaga	1740
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atcagggact	cgtatcaatt	atcctgacta	agtcaacggg	gggcggtgtc	gagaagacca	1860
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ccgctgttcc	tataatacct	gttaattacg	attcggatcc	gaaactgaat	tcacagttat	1980
atacggttga	gatgacgac	cctgcagggtg	taagcgcagt	taaaatcgta	ccaacagata	2040
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gatccttttc	tgtcaaagag	aatacgtcat	acacattctc	agcaatttat	actggtggcg	2220
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acagcaatga	caataaacia	agaacagaaa	tagcgactaa	aaacttccca	gtatcaacga	2340
ctatttcaaa	aagttttttt	gcgcctgaac	cacaaatcca	gccttctttt	ggtaaaaatg	2400
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ctgatgatcc	ccaatcaata	atctaccaga	ttggtgatga	taaagggaaa	aaaatgttaa	2580
aagatcatgg	tacagagggt	acgcctaatac	aacaaataac	ttttaaagcg	ctgaattata	2640

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ctagcggaga taaagaaata cctcctggga tatataacga tcaggttatg gttggttact 2700  
 acgtaaacga caataaacaa ggaactggc aatataaatc tctggatgta aatgtaaata 2760  
 ttgagcaact cgagcaccac caccaccacc actga 2795

<210> SEQ ID NO 27  
 <211> LENGTH: 963  
 <212> TYPE: PRT  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 27

Met Gly Arg Tyr Pro Glu Thr Thr Val Gly Asn Leu Thr Lys Ser Phe  
 1 5 10 15  
 Gln Ala Pro Arg Gln Asp Arg Ser Val Gln Ser Pro Ile Tyr Asn Ile  
 20 25 30  
 Phe Thr Asn His Val Ala Gly Tyr Ser Leu Ser His Asn Leu Tyr Asp  
 35 40 45  
 Arg Ile Val Phe Leu Cys Thr Ser Ser Ser Asn Pro Val Asn Gly Ala  
 50 55 60  
 Cys Pro Thr Ile Gly Thr Ser Gly Val Gln Tyr Gly Thr Thr Thr Ile  
 65 70 75 80  
 Thr Leu Gln Phe Thr Glu Lys Arg Ser Leu Ile Lys Arg Asn Ile Asn  
 85 90 95  
 Leu Ala Gly Asn Lys Lys Pro Ile Trp Glu Asn Gln Ser Cys Asp Thr  
 100 105 110  
 Ser Asn Leu Met Val Leu Asn Ser Lys Ser Trp Ser Cys Gly Ala Tyr  
 115 120 125  
 Gly Asn Ala Asn Gly Thr Leu Leu Asn Leu Tyr Ile Pro Ala Gly Glu  
 130 135 140  
 Ile Asn Lys Leu Pro Phe Gly Gly Ile Trp Glu Ala Thr Leu Ile Leu  
 145 150 155 160  
 Arg Leu Ser Arg Tyr Gly Glu Val Ser Ser Thr His Tyr Gly Asn Tyr  
 165 170 175  
 Thr Val Asn Ile Thr Val Asp Leu Thr Asp Lys Gly Asn Ile Gln Val  
 180 185 190  
 Trp Leu Pro Gly Phe His Ser Asn Pro Arg Val Asp Leu Asn Leu His  
 195 200 205  
 Pro Ile Gly Asn Tyr Lys Tyr Ser Gly Ser Asn Ser Leu Asp Met Cys  
 210 215 220  
 Phe Tyr Asp Gly Tyr Ser Thr Asn Ser Asp Ser Met Val Ile Lys Phe  
 225 230 235 240  
 Gln Asp Asp Asn Pro Thr Tyr Ser Ser Glu Tyr Asn Leu Tyr Lys Ile  
 245 250 255  
 Gly Gly Thr Glu Lys Leu Pro Tyr Ala Val Ser Leu Leu Met Gly Glu  
 260 265 270  
 Lys Ile Phe Tyr Pro Val Asn Gly Gln Ser Phe Thr Ile Asn Asp Ser  
 275 280 285  
 Ser Val Leu Glu Thr Asn Trp Asn Arg Val Thr Ala Val Ala Met Pro  
 290 295 300  
 Glu Val Asn Val Pro Val Leu Cys Trp Pro Ala Arg Leu Leu Leu Asn  
 305 310 315 320  
 Ala Asp Val Asn Ala Pro Asp Ala Gly Gln Tyr Ser Gly Gln Ile Tyr  
 325 330 335  
 Ile Thr Phe Thr Pro Ser Val Glu Asn Leu Gly Gly Gly Val Glu Lys  
 340 345 350



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Tyr Thr Gly Gly Glu Tyr Pro Asn Ser Gly Tyr Ser Ser Gly Thr Tyr  
 770 775 780

Ala Gly His Leu Thr Val Ser Phe Tyr Ser Asn Asp Asn Lys Gln Arg  
 785 790 795 800

Thr Glu Ile Ala Thr Lys Asn Phe Pro Val Ser Thr Thr Ile Ser Lys  
 805 810 815

Ser Phe Phe Ala Pro Glu Pro Gln Ile Gln Pro Ser Phe Gly Lys Asn  
 820 825 830

Val Gly Lys Glu Gly Asp Leu Leu Phe Ser Val Ser Leu Ile Val Pro  
 835 840 845

Glu Asn Val Ser Gln Val Thr Val Tyr Pro Val Tyr Asp Glu Asp Tyr  
 850 855 860

Gly Leu Gly Arg Leu Val Asn Thr Ala Asp Asp Ser Gln Ser Ile Ile  
 865 870 875 880

Tyr Gln Ile Val Asp Asp Lys Gly Lys Lys Met Leu Lys Asp His Gly  
 885 890 895

Thr Glu Val Thr Pro Asn Gln Gln Ile Thr Phe Lys Ala Leu Asn Tyr  
 900 905 910

Thr Ser Gly Asp Lys Glu Ile Pro Pro Gly Ile Tyr Asn Asp Gln Val  
 915 920 925

Met Val Gly Tyr Tyr Val Asn Asp Asn Lys Gln Gly Asn Trp Gln Tyr  
 930 935 940

Lys Ser Leu Asp Val Asn Val Asn Ile Glu Gln Leu Glu His His His  
 945 950 955 960

His His His

<210> SEQ ID NO 28  
 <211> LENGTH: 2505  
 <212> TYPE: DNA  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 28

atgaaaaaag tgatttttgt tttatccatg tttctatggt ctcaggttta cgggcaatca 60

tggcatacga acgtagaggc tggttcaata aataaaacag agtcgatagg ccccatagac 120

cgaagtgctg ctgcatcgta tctctgctcat tatatatttc atgaacatgt tgctggttac 180

aataaagatc actctctttt tgacaggatg acgtttttat gtatgtcatc aacagatgca 240

tctaaagggt catgtccgac aggagaaaac tccaaatcct ctcaagggga gactaatatt 300

aagctaatat ttactgaaaa gaaaagtctg gccagaaaaa cattaaactt aaaaggatat 360

aagagatttt tatatgaatc agatagatgc attcattatg tcgataaaat gaatctcaat 420

tctcactctg ttaaatgtgt aggttcattc acaagaggag tagatttcac tttatatatc 480

ccacaagggt aaattgatgg gcttctaact ggaggtatat gggaggcaac actagagtta 540

cgagtcaaaa ggcattaacga ctataatcat ggtacttaca aagttaatat cacagttgat 600

ttgacagaca aaggaaatat tcaggtctgg acaccaaagt ttcatagcga tcctagaatt 660

gatctgaatt tacgtctcga aggtaatggt aaatattctg gtagtaacgt gcttgagatg 720

tgtctctatg atggctatag tacacatagt caaagtatag aaatgagggt tcaggatgac 780

tcacaaacag gaaataatga atataatctt ataaaaactg gagagccatt aaaaaaattg 840

ccatataaac tttctcttct tttaggagga cgagagtttt atccaaataa tggagagget 900

tttactatta atgatacttc gtcattggtt ataaactgga atcgtattaa gtctgtatcc 960

ttaccacaga ttagtattcc agtactatgc tggccagcaa acttgacatt tatgtcagag 1020

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ctaaataatc cagaagcggg tgagtattca ggaataactta acgtaacatt tactcctagt 1080
agttcaagcc tagacaataa acaagccgag aaaaatatca ctgtaactgc tagcgttgat 1140
ccaactatcg atctgatgca atctgatggc acagcgttac caagtgcagt taatattgca 1200
tatcttcag gagagaaaag atttgaatct gctcgtatca ataccaagt tcataccaat 1260
aataaaacta agggatttca gataaagctt actaatgata atgtggtaat gactaactta 1320
tctgatccaa gcaagactat tccttttagag gtttcattcg ctggcactaa gctgagcaca 1380
gctgcaacat ctattactgc cgatcaatta aatttggcg cagctgggtg agagacagtt 1440
tctgcaacta aggaactcgt tattaatgca ggaagcacc agcaactaa tattgtagct 1500
ggtaactatc aaggattggg gtcaatttg gttactcaag aacctgacaa taaacaagcc 1560
gagaaaaata tcaactgtaac tgctagcgtt gatccgacgg gcgagcaaaa ttttattcca 1620
gatattgatt ccgctgttcg tataatacct gtaattacg attcggatcc gaaactgaat 1680
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ccagatcaaa atatgaatta ttatatcaga aaggattctg gcgctggtaa gtttatggca 1860
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aaaatgtaa aagatcatgg tacagagggt acgcctaate aacaataaac ttttaagcg 2340
ctgaattata ctagcggaga taaagaata cctcctggga tatataacga tcaggttatg 2400
gttggttact acgtaaaca caataaaca ggaactggc aatataaatc tctggatgta 2460
aatgtaaata ttgagcaact cgagcaccac caccaccacc actga 2505

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<210> SEQ ID NO 29
<211> LENGTH: 834
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

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<400> SEQUENCE: 29

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Met Lys Lys Val Ile Phe Val Leu Ser Met Phe Leu Cys Ser Gln Val
1           5           10           15
Tyr Gly Gln Ser Trp His Thr Asn Val Glu Ala Gly Ser Ile Asn Lys
20          25          30
Thr Glu Ser Ile Gly Pro Ile Asp Arg Ser Ala Ala Ala Ser Tyr Pro
35          40          45
Ala His Tyr Ile Phe His Glu His Val Ala Gly Tyr Asn Lys Asp His
50          55          60
Ser Leu Phe Asp Arg Met Thr Phe Leu Cys Met Ser Ser Thr Asp Ala
65          70          75          80
Ser Lys Gly Ala Cys Pro Thr Gly Glu Asn Ser Lys Ser Ser Gln Gly
85          90          95
Glu Thr Asn Ile Lys Leu Ile Phe Thr Glu Lys Lys Ser Leu Ala Arg
100         105         110

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Lys Thr Leu Asn Leu Lys Gly Tyr Lys Arg Phe Leu Tyr Glu Ser Asp  
 115 120 125  
 Arg Cys Ile His Tyr Val Asp Lys Met Asn Leu Asn Ser His Thr Val  
 130 135 140  
 Lys Cys Val Gly Ser Phe Thr Arg Gly Val Asp Phe Thr Leu Tyr Ile  
 145 150 155 160  
 Pro Gln Gly Glu Ile Asp Gly Leu Leu Thr Gly Gly Ile Trp Glu Ala  
 165 170 175  
 Thr Leu Glu Leu Arg Val Lys Arg His Tyr Asp Tyr Asn His Gly Thr  
 180 185 190  
 Tyr Lys Val Asn Ile Thr Val Asp Leu Thr Asp Lys Gly Asn Ile Gln  
 195 200 205  
 Val Trp Thr Pro Lys Phe His Ser Asp Pro Arg Ile Asp Leu Asn Leu  
 210 215 220  
 Arg Pro Glu Gly Asn Gly Lys Tyr Ser Gly Ser Asn Val Leu Glu Met  
 225 230 235 240  
 Cys Leu Tyr Asp Gly Tyr Ser Thr His Ser Gln Ser Ile Glu Met Arg  
 245 250 255  
 Phe Gln Asp Asp Ser Gln Thr Gly Asn Asn Glu Tyr Asn Leu Ile Lys  
 260 265 270  
 Thr Gly Glu Pro Leu Lys Lys Leu Pro Tyr Lys Leu Ser Leu Leu Leu  
 275 280 285  
 Gly Gly Arg Glu Phe Tyr Pro Asn Asn Gly Glu Ala Phe Thr Ile Asn  
 290 295 300  
 Asp Thr Ser Ser Leu Phe Ile Asn Trp Asn Arg Ile Lys Ser Val Ser  
 305 310 315 320  
 Leu Pro Gln Ile Ser Ile Pro Val Leu Cys Trp Pro Ala Asn Leu Thr  
 325 330 335  
 Phe Met Ser Glu Leu Asn Asn Pro Glu Ala Gly Glu Tyr Ser Gly Ile  
 340 345 350  
 Leu Asn Val Thr Phe Thr Pro Ser Ser Ser Ser Leu Asp Asn Lys Gln  
 355 360 365  
 Ala Glu Lys Asn Ile Thr Val Thr Ala Ser Val Asp Pro Thr Ile Asp  
 370 375 380  
 Leu Met Gln Ser Asp Gly Thr Ala Leu Pro Ser Ala Val Asn Ile Ala  
 385 390 395 400  
 Tyr Leu Pro Gly Glu Lys Arg Phe Glu Ser Ala Arg Ile Asn Thr Gln  
 405 410 415  
 Val His Thr Asn Asn Lys Thr Lys Gly Ile Gln Ile Lys Leu Thr Asn  
 420 425 430  
 Asp Asn Val Val Met Thr Asn Leu Ser Asp Pro Ser Lys Thr Ile Pro  
 435 440 445  
 Leu Glu Val Ser Phe Ala Gly Thr Lys Leu Ser Thr Ala Ala Thr Ser  
 450 455 460  
 Ile Thr Ala Asp Gln Leu Asn Phe Gly Ala Ala Gly Val Glu Thr Val  
 465 470 475 480  
 Ser Ala Thr Lys Glu Leu Val Ile Asn Ala Gly Ser Thr Gln Gln Thr  
 485 490 495  
 Asn Ile Val Ala Gly Asn Tyr Gln Gly Leu Val Ser Ile Val Leu Thr  
 500 505 510  
 Gln Glu Pro Asp Asn Lys Gln Ala Glu Lys Asn Ile Thr Val Thr Ala  
 515 520 525

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Ser Val Asp Pro Thr Gly Glu Gln Asn Phe Ile Pro Asp Ile Asp Ser  
 530 535 540

Ala Val Arg Ile Ile Pro Val Asn Tyr Asp Ser Asp Pro Lys Leu Asn  
 545 550 555 560

Ser Gln Leu Tyr Thr Val Glu Met Thr Ile Pro Ala Gly Val Ser Ala  
 565 570 575

Val Lys Ile Val Pro Thr Asp Ser Leu Thr Ser Ser Gly Gln Gln Ile  
 580 585 590

Gly Lys Leu Val Asn Val Asn Asn Pro Asp Gln Asn Met Asn Tyr Tyr  
 595 600 605

Ile Arg Lys Asp Ser Gly Ala Gly Lys Phe Met Ala Gly Gln Lys Gly  
 610 615 620

Ser Phe Ser Val Lys Glu Asn Thr Ser Tyr Thr Phe Ser Ala Ile Tyr  
 625 630 635 640

Thr Gly Gly Glu Tyr Pro Asn Ser Gly Tyr Ser Ser Gly Thr Tyr Ala  
 645 650 655

Gly His Leu Thr Val Ser Phe Tyr Ser Asn Asp Asn Lys Gln Arg Thr  
 660 665 670

Glu Ile Ala Thr Lys Asn Phe Pro Val Ser Thr Thr Ile Ser Lys Ser  
 675 680 685

Phe Phe Ala Pro Glu Pro Gln Ile Gln Pro Ser Phe Gly Lys Asn Val  
 690 695 700

Gly Lys Glu Gly Asp Leu Leu Phe Ser Val Ser Leu Ile Val Pro Glu  
 705 710 715 720

Asn Val Ser Gln Val Thr Val Tyr Pro Val Tyr Asp Glu Asp Tyr Gly  
 725 730 735

Leu Gly Arg Leu Val Asn Thr Ala Asp Asp Ser Gln Ser Ile Ile Tyr  
 740 745 750

Gln Ile Val Asp Asp Lys Gly Lys Lys Met Leu Lys Asp His Gly Thr  
 755 760 765

Glu Val Thr Pro Asn Gln Gln Ile Thr Phe Lys Ala Leu Asn Tyr Thr  
 770 775 780

Ser Gly Asp Lys Glu Ile Pro Pro Gly Ile Tyr Asn Asp Gln Val Met  
 785 790 795 800

Val Gly Tyr Tyr Val Asn Asp Asn Lys Gln Gly Asn Trp Gln Tyr Lys  
 805 810 815

Ser Leu Asp Val Asn Val Asn Ile Glu Gln Leu Glu His His His His  
 820 825 830

His His

<210> SEQ ID NO 30  
 <211> LENGTH: 2454  
 <212> TYPE: DNA  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 30

atgcaatcat ggcatacga cgtagaggct ggttcaataa ataaaacaga gtcgataggc 60  
 cccatagacc gaagtgtgc tgcacgtat cctgctcatt atatatttca tgaacatggt 120  
 gctggttaca ataaagatca ctctcttttt gacaggatga cgtttttatg tatgtcatca 180  
 acagatgcat ctaaagggtgc atgtccgaca ggagaaaact ccaaatcctc tcaaggggag 240  
 actaatatta agctaattatt tactgaaaag aaaagtctgg ccagaaaaac attaaactta 300  
 aaaggatata agagattttt atatgaatca gatagatgca ttcattatgt cgataaaatg 360

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aatctcaatt ctcatactgt taaatgtgta ggttcattca caagaggagt agatttcaact 420
ttatatatcc cacaagggtga aattgatggg cttctaactg gaggtatatg ggaggcaaca 480
ctagagttac gagtcaaaag gcattacgac tataatcatg gtacttacia agttaatatc 540
acagttgatt tgacagacaa aggaaatatt caggtctgga caccaaagtt tcatagcgat 600
cctagaattg atctgaattt acgtcctgaa ggtaatggta aatattctgg tagtaacgtg 660
cttgagatgt gtctctatga tggctatagt acacatagtc aaagtataga aatgaggttt 720
caggatgact cacaaacagg aaataatgaa tataatctta taaaaactgg agagccatta 780
aaaaaattgc catataaact ttctcttctt ttagggaggac gagagtttta tccaaataat 840
ggagaggcct ttactattaa tgatacttcg tcattgttta taaactggaa tcgtattaag 900
tctgtatcct taccacagat tagtattcca gtactatgct ggccagcaaa cttgacattt 960
atgtcagagc taaataatcc agaagcgggt gagtattcag gaataactaa cgtaacattt 1020
actcctagta gttcaagcct agacaataaa caagccgaga aaaatatcac tgtaactgct 1080
agcgttgatc caactatcga tctgatgcaa tctgatggca cagcgttacc aagtgcagtt 1140
aatattgcat atcttccagg agagaaaaga ttggaactcg ctctatcaa tacccaagtt 1200
cataccaata ataaaaactaa gggatttcag ataaagctta ctaatgataa tgtggtaatg 1260
actaacttat ctgatccaag caagactatt cctttagagg ttctattcgc tggcactaag 1320
ctgagcacag ctgcaacatc tattactgcc gatcaattaa attttggcgc agctggtgta 1380
gagacagttt ctgcaactaa ggaactcgtt attaatgcag gaagcaccca gcaaaactaa 1440
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aaacaagccg agaaaaatat cactgtaact gctagcgttg atccgacggg cgagcaaat 1560
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aaactgaatt cacagttata tacggttgag atgacgatcc ctgcaggtgt aagcgcagtt 1680
aaaatcgtac caacagatag tctgacatct tctggacagc agatcggaaa gctggttaat 1740
gtaaacaaac cagatcaaaa tatgaattat tatatcagaa aggattctgg cgctggtaag 1800
tttatggcag ggcaaaaagg atccttttct gtcaaagaga atacgtcata cacattctca 1860
gcaatttata ctggtggcga atacccta atgcggatatt cgtctggtac ttatgcagga 1920
catttgactg tatcatttta cagcaatgac aataaacaaa gaacagaaat agcgcactaaa 1980
aacttcccag tatcaacgac tatttcaaaa agtttttttg cgcctgaacc acaaatccag 2040
ccttcttttg gtaaaaatgt tggaaaggaa ggagatttat tatttagtgt gagcttaatt 2100
gttctgaaa atgtatccca ggtaacggtc taccctgttt atgatgaaga ttatggatta 2160
ggacgactcg taaataccgc tgatgattcc caatcaataa tctaccagat tgttgatgat 2220
aaagggaaaa aaatgttaaa agatcatggt acagaggtta cgcctaataca acaataaact 2280
tttaaagcgc tgaattatac tagcggagat aaagaaatac ctctgggat atataacgat 2340
caggttatgg ttggttacta cgtaaaocgac aataaacaag gaaactggca atataaatct 2400
ctggatgtaa atgtaaatat tgagcaactc gagcaccacc accaccacca ctga 2454

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&lt;210&gt; SEQ ID NO 31

&lt;211&gt; LENGTH: 817

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Escherichia coli

&lt;400&gt; SEQUENCE: 31

Met Gln Ser Trp His Thr Asn Val Glu Ala Gly Ser Ile Asn Lys Thr

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1	5	10	15
Glu Ser Ile Gly Pro Ile Asp Arg Ser Ala Ala Ala Ser Tyr Pro Ala	20	25	30
His Tyr Ile Phe His Glu His Val Ala Gly Tyr Asn Lys Asp His Ser	35	40	45
Leu Phe Asp Arg Met Thr Phe Leu Cys Met Ser Ser Thr Asp Ala Ser	50	55	60
Lys Gly Ala Cys Pro Thr Gly Glu Asn Ser Lys Ser Ser Gln Gly Glu	65	70	80
Thr Asn Ile Lys Leu Ile Phe Thr Glu Lys Lys Ser Leu Ala Arg Lys	85	90	95
Thr Leu Asn Leu Lys Gly Tyr Lys Arg Phe Leu Tyr Glu Ser Asp Arg	100	105	110
Cys Ile His Tyr Val Asp Lys Met Asn Leu Asn Ser His Thr Val Lys	115	120	125
Cys Val Gly Ser Phe Thr Arg Gly Val Asp Phe Thr Leu Tyr Ile Pro	130	135	140
Gln Gly Glu Ile Asp Gly Leu Leu Thr Gly Gly Ile Trp Glu Ala Thr	145	150	160
Leu Glu Leu Arg Val Lys Arg His Tyr Asp Tyr Asn His Gly Thr Tyr	165	170	175
Lys Val Asn Ile Thr Val Asp Leu Thr Asp Lys Gly Asn Ile Gln Val	180	185	190
Trp Thr Pro Lys Phe His Ser Asp Pro Arg Ile Asp Leu Asn Leu Arg	195	200	205
Pro Glu Gly Asn Gly Lys Tyr Ser Gly Ser Asn Val Leu Glu Met Cys	210	215	220
Leu Tyr Asp Gly Tyr Ser Thr His Ser Gln Ser Ile Glu Met Arg Phe	225	230	240
Gln Asp Asp Ser Gln Thr Gly Asn Asn Glu Tyr Asn Leu Ile Lys Thr	245	250	255
Gly Glu Pro Leu Lys Lys Leu Pro Tyr Lys Leu Ser Leu Leu Leu Gly	260	265	270
Gly Arg Glu Phe Tyr Pro Asn Asn Gly Glu Ala Phe Thr Ile Asn Asp	275	280	285
Thr Ser Ser Leu Phe Ile Asn Trp Asn Arg Ile Lys Ser Val Ser Leu	290	295	300
Pro Gln Ile Ser Ile Pro Val Leu Cys Trp Pro Ala Asn Leu Thr Phe	305	310	320
Met Ser Glu Leu Asn Asn Pro Glu Ala Gly Glu Tyr Ser Gly Ile Leu	325	330	335
Asn Val Thr Phe Thr Pro Ser Ser Ser Ser Leu Asp Asn Lys Gln Ala	340	345	350
Glu Lys Asn Ile Thr Val Thr Ala Ser Val Asp Pro Thr Ile Asp Leu	355	360	365
Met Gln Ser Asp Gly Thr Ala Leu Pro Ser Ala Val Asn Ile Ala Tyr	370	375	380
Leu Pro Gly Glu Lys Arg Phe Glu Ser Ala Arg Ile Asn Thr Gln Val	385	390	400
His Thr Asn Asn Lys Thr Lys Gly Ile Gln Ile Lys Leu Thr Asn Asp	405	410	415
Asn Val Val Met Thr Asn Leu Ser Asp Pro Ser Lys Thr Ile Pro Leu	420	425	430



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&lt;213&gt; ORGANISM: Escherichia coli

&lt;400&gt; SEQUENCE: 32

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agcgttgttg atggtcgcca gactggtttt tttaccttca tggactcadc agccacttac    240
aaaattagta caaaactggg atcatcgaat gatgtaaaaca ttcaagaaat tactcaagga    300
gctaaaaata ctctgttag tggagagaaa actttgccta aaaaattcac tcttaagcta    360
catgcacaca ggagtagcag tacagtcca ggtacgtata ctgttggtct taacgtaacc    420
agtaacgtta ttgataacaa gcaggcagcg gggcccactc taaccaaaga actggcatta    480
aatgtgcttt ctctgcagc tctggatgca acttgggctc ctccaggataa tttaacatta    540
tccaatactg gcgtttctaa tactttggty ggtgttttga ctctttcaaa taccagtatt    600
gatacagtta gcattgcgag taaaaatgtt tctgatacat ctaagaatgg tacagtaact    660
tttgcacatg agacaaataa ctctgctagc ttgcccacca ccatttcaac agataatgcc    720
aacattacgt tggataaaaa tgtcggaaat acgattgtta aaactacaaa tgggagtcag    780
ttgccaacta atttaccact taagtttatt accactgaag gtaacgaaca tttagtttca    840
ggtaattacc gtgcaaatat aacaattact tcgacaatta aagataacaa gcaggcggca    900
ggtccaaccc tgactaagga gttagcgtg aacgttttaa gcggcgagca aaattttatt    960
ccagatattg attccgctgt tcgtataata cctgttaatt acgattcggg tccgaaactg   1020
aattcacagt tatacaggt tgagatgacg atccctgcag gtgtaagcgc agttaaatac   1080
gtaccaacag atagtctgac atcttctgga cagcagatcg gaaagctggt taatgtaaac   1140
aatccagatc aaaatatgaa ttattatctc agaaaggatt ctggcgctgg taagtttatg   1200
gcagggcaaa aaggatcctt tctgtcmeta gagaatacgt catacacatt ctacgcaatt   1260
tatactggty gcgaataacc taatagcggg tattcgtctg gtacttatgc aggacatttg   1320
actgtatcat tttacagcaa tgacaataaa caaagaacag aaatagcgc taaaaacttc   1380
ccagtatcaa cgactatttc aaaaagtfff ttgvcgctg aaccacaaat ccagccttct   1440
tttggtaaaa atgttggaag ggaaggagat ttattattha gtgtgagctt aattgttctc   1500
gaaaatgtat cccaggtaac ggtctaccct gtttatgatg aagattatgg attaggacga   1560
ctcgtaaata ccgctgatga ttcccaatca ataactacc agattgttga tgataaaggg   1620
aaaaaaaaatg taaaagatca tggtagcagag gttacgccta atcaacaaat aacttttaaa   1680
gcgctgaatt atactagcgg agataaagaa atacctcctg ggatatataa cgatcaggtt   1740
atggttggtt actacgtaaa cgacaataaa caaggaaact ggcaatataa atctctggat   1800
gtaaatgtaa atattgagca actcagagcac caccaccacc accactga    1848

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&lt;210&gt; SEQ ID NO 33

&lt;211&gt; LENGTH: 615

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Escherichia coli

&lt;400&gt; SEQUENCE: 33

```

Met Ala Val Gly Pro Thr Lys Asp Met Ser Leu Gly Ala Asn Leu Thr
 1             5             10             15
Ser Glu Pro Thr Leu Ala Ile Asp Phe Thr Pro Ile Glu Asn Ile Tyr
          20             25             30

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Val Gly Ala Asn Tyr Gly Lys Asp Ile Gly Thr Leu Val Phe Thr Thr  
 35 40 45  
 Asn Asp Leu Thr Asp Ile Thr Leu Met Ser Ser Arg Ser Val Val Asp  
 50 55 60  
 Gly Arg Gln Thr Gly Phe Phe Thr Phe Met Asp Ser Ser Ala Thr Tyr  
 65 70 75 80  
 Lys Ile Ser Thr Lys Leu Gly Ser Ser Asn Asp Val Asn Ile Gln Glu  
 85 90 95  
 Ile Thr Gln Gly Ala Lys Ile Thr Pro Val Ser Gly Glu Lys Thr Leu  
 100 105 110  
 Pro Lys Lys Phe Thr Leu Lys Leu His Ala His Arg Ser Ser Ser Thr  
 115 120 125  
 Val Pro Gly Thr Tyr Thr Val Gly Leu Asn Val Thr Ser Asn Val Ile  
 130 135 140  
 Asp Asn Lys Gln Ala Ala Gly Pro Thr Leu Thr Lys Glu Leu Ala Leu  
 145 150 155 160  
 Asn Val Leu Ser Pro Ala Ala Leu Asp Ala Thr Trp Ala Pro Gln Asp  
 165 170 175  
 Asn Leu Thr Leu Ser Asn Thr Gly Val Ser Asn Thr Leu Val Gly Val  
 180 185 190  
 Leu Thr Leu Ser Asn Thr Ser Ile Asp Thr Val Ser Ile Ala Ser Thr  
 195 200 205  
 Asn Val Ser Asp Thr Ser Lys Asn Gly Thr Val Thr Phe Ala His Glu  
 210 215 220  
 Thr Asn Asn Ser Ala Ser Phe Ala Thr Thr Ile Ser Thr Asp Asn Ala  
 225 230 235 240  
 Asn Ile Thr Leu Asp Lys Asn Ala Gly Asn Thr Ile Val Lys Thr Thr  
 245 250 255  
 Asn Gly Ser Gln Leu Pro Thr Asn Leu Pro Leu Lys Phe Ile Thr Thr  
 260 265 270  
 Glu Gly Asn Glu His Leu Val Ser Gly Asn Tyr Arg Ala Asn Ile Thr  
 275 280 285  
 Ile Thr Ser Thr Ile Lys Asp Asn Lys Gln Ala Ala Gly Pro Thr Leu  
 290 295 300  
 Thr Lys Glu Leu Ala Leu Asn Val Leu Ser Gly Glu Gln Asn Phe Ile  
 305 310 315 320  
 Pro Asp Ile Asp Ser Ala Val Arg Ile Ile Pro Val Asn Tyr Asp Ser  
 325 330 335  
 Asp Pro Lys Leu Asn Ser Gln Leu Tyr Thr Val Glu Met Thr Ile Pro  
 340 345 350  
 Ala Gly Val Ser Ala Val Lys Ile Val Pro Thr Asp Ser Leu Thr Ser  
 355 360 365  
 Ser Gly Gln Gln Ile Gly Lys Leu Val Asn Val Asn Asn Pro Asp Gln  
 370 375 380  
 Asn Met Asn Tyr Tyr Ile Arg Lys Asp Ser Gly Ala Gly Lys Phe Met  
 385 390 395 400  
 Ala Gly Gln Lys Gly Ser Phe Ser Val Lys Glu Asn Thr Ser Tyr Thr  
 405 410 415  
 Phe Ser Ala Ile Tyr Thr Gly Gly Glu Tyr Pro Asn Ser Gly Tyr Ser  
 420 425 430  
 Ser Gly Thr Tyr Ala Gly His Leu Thr Val Ser Phe Tyr Ser Asn Asp  
 435 440 445

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Asn Lys Gln Arg Thr Glu Ile Ala Thr Lys Asn Phe Pro Val Ser Thr  
 450 455 460

Thr Ile Ser Lys Ser Phe Phe Ala Pro Glu Pro Gln Ile Gln Pro Ser  
 465 470 475 480

Phe Gly Lys Asn Val Gly Lys Glu Gly Asp Leu Leu Phe Ser Val Ser  
 485 490 495

Leu Ile Val Pro Glu Asn Val Ser Gln Val Thr Val Tyr Pro Val Tyr  
 500 505 510

Asp Glu Asp Tyr Gly Leu Gly Arg Leu Val Asn Thr Ala Asp Asp Ser  
 515 520 525

Gln Ser Ile Ile Tyr Gln Ile Val Asp Asp Lys Gly Lys Lys Met Leu  
 530 535 540

Lys Asp His Gly Thr Glu Val Thr Pro Asn Gln Gln Ile Thr Phe Lys  
 545 550 555 560

Ala Leu Asn Tyr Thr Ser Gly Asp Lys Glu Ile Pro Pro Gly Ile Tyr  
 565 570 575

Asn Asp Gln Val Met Val Gly Tyr Tyr Val Asn Asp Asn Lys Gln Gly  
 580 585 590

Asn Trp Gln Tyr Lys Ser Leu Asp Val Asn Val Asn Ile Glu Gln Leu  
 595 600 605

Glu His His His His His His  
 610 615

<210> SEQ ID NO 34  
 <211> LENGTH: 1794  
 <212> TYPE: DNA  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 34

```

atggagcaaa attttattcc agatattgat tccgctgttc gtataatacc tgttaattac    60
gattcggatc cgaaaactgaa ttcacagtta tatacggttg agatgacgat ccttgcaggt    120
gtaagcgcag ttaaaatcgt accaacagat agtctgacat cttctggaca gcagatcgga    180
aagctgggta atgtaaacia tccagatcaa aatatgaatt attatatcag aaaggattct    240
ggcgtgggta agtttatggc agggcaaaaa ggatcctttt ctgtcaaaga gaatacgtca    300
tacacattct cagcaattta tactgggtggc gaatacccta atagcggata ttcgtctggt    360
acttatgcag gacatttgac tgtatcattt tacagcaatg acaataaaca aagaacagaa    420
atagcggacta aaaacttccc agtatcaacg actatttcaa aaagtttttt tgcgcctgaa    480
ccacaaatcc agccttcttt tggtaaaaat gttgaaagg aaggagattt attatttagt    540
gtgagcctaa ttgttcctga aaatgtatcc caggtaacgg tctaccctgt ttatgatgaa    600
gattatggat taggacgact cgtaaatacc gctgatgatt cccaatcaat aatctaccag    660
attgttgatg ataaagggaa aaaaatgtta aaagatcatg gtacagaggt tacgcctaata    720
caacaaataa cttttaaagc gctgaattat actagcggag ataaagaaat acctcctggg    780
atatataacg atcaggttat ggttggttac tacgtaaacg acaataaaca aggaaactgg    840
caatataaat ctctggacgt gaatgtaaata attgagcaag gcacattagc tattgatttt    900
acgcctattg aaaatattta tgtaggtgcc aattatggta aagatattgg aacccttggt    960
ttcacaacaa atgatttaac agatattaca ttgatgtcat ctcgcagcgt tgttgatggt    1020
cgccagactg gtttttttac cttcatggac tcatcagcca cttacaaaat tagtacaaaa    1080
ctgggatcat cgaatgatgt aaacattcaa gaaattactc aaggagctaa aattactcct    1140
    
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gttagtggag agaaaacttt gcctaaaaa ttcactctta agctacatgc acacaggagt 1200
agcagtacag ttccaggtag gtatactggt ggtcttaacg taaccagtaa cgttattgat 1260
aacaagcagg cagcggggcc cactctaacc aaagaactgg cattaatgt gctttctcct 1320
gcagctctgg atgcaacttg ggctcctcag gataatttaa cattatccaa tactggcggt 1380
tctaatactt tgggtgggtgt tttgactctt tcaaatacca gtattgatac agttagcatt 1440
gcgagtacaa atgtttctga tacatctaag aatggtacag taacttttgc acatgagaca 1500
aataactctg ctagctttgc caccaccatt tcaacagata atgccaacat tacgttggat 1560
aaaaatgctg gaaatacgat tgtaaact acaaatggga gtcagttgcc aactaattha 1620
ccacttaagt ttattaccac tgaaggtaac gaacatttag tttcaggtaa ttaccgtgca 1680
aatataacaa ttacttcgac aattaaagat aacaagcagg cggcaggtcc aacctgact 1740
aaggagttag cgctgaacgt tctgagcctc gagcaccacc accaccacca ctga 1794

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&lt;210&gt; SEQ ID NO 35

&lt;211&gt; LENGTH: 597

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Escherichia coli

&lt;400&gt; SEQUENCE: 35

```

Met Glu Gln Asn Phe Ile Pro Asp Ile Asp Ser Ala Val Arg Ile Ile
1           5           10           15
Pro Val Asn Tyr Asp Ser Asp Pro Lys Leu Asn Ser Gln Leu Tyr Thr
20          25          30
Val Glu Met Thr Ile Pro Ala Gly Val Ser Ala Val Lys Ile Val Pro
35          40          45
Thr Asp Ser Leu Thr Ser Ser Gly Gln Gln Ile Gly Lys Leu Val Asn
50          55          60
Val Asn Asn Pro Asp Gln Asn Met Asn Tyr Tyr Ile Arg Lys Asp Ser
65          70          75          80
Gly Ala Gly Lys Phe Met Ala Gly Gln Lys Gly Ser Phe Ser Val Lys
85          90          95
Glu Asn Thr Ser Tyr Thr Phe Ser Ala Ile Tyr Thr Gly Gly Glu Tyr
100         105         110
Pro Asn Ser Gly Tyr Ser Ser Gly Thr Tyr Ala Gly His Leu Thr Val
115         120         125
Ser Phe Tyr Ser Asn Asp Asn Lys Gln Arg Thr Glu Ile Ala Thr Lys
130         135         140
Asn Phe Pro Val Ser Thr Thr Ile Ser Lys Ser Phe Phe Ala Pro Glu
145         150         155         160
Pro Gln Ile Gln Pro Ser Phe Gly Lys Asn Val Gly Lys Glu Gly Asp
165         170         175
Leu Leu Phe Ser Val Ser Leu Ile Val Pro Glu Asn Val Ser Gln Val
180         185         190
Thr Val Tyr Pro Val Tyr Asp Glu Asp Tyr Gly Leu Gly Arg Leu Val
195         200         205
Asn Thr Ala Asp Asp Ser Gln Ser Ile Ile Tyr Gln Ile Val Asp Asp
210         215         220
Lys Gly Lys Lys Met Leu Lys Asp His Gly Thr Glu Val Thr Pro Asn
225         230         235         240
Gln Gln Ile Thr Phe Lys Ala Leu Asn Tyr Thr Ser Gly Asp Lys Glu
245         250         255
Ile Pro Pro Gly Ile Tyr Asn Asp Gln Val Met Val Gly Tyr Tyr Val

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260				265				270							
Asn	Asp	Asn	Lys	Gln	Gly	Asn	Trp	Gln	Tyr	Lys	Ser	Leu	Asp	Val	Asn
	275						280						285		
Val	Asn	Ile	Glu	Gln	Gly	Thr	Leu	Ala	Ile	Asp	Phe	Thr	Pro	Ile	Glu
	290						295				300				
Asn	Ile	Tyr	Val	Gly	Ala	Asn	Tyr	Gly	Lys	Asp	Ile	Gly	Thr	Leu	Val
	305				310					315					320
Phe	Thr	Thr	Asn	Asp	Leu	Thr	Asp	Ile	Thr	Leu	Met	Ser	Ser	Arg	Ser
			325						330					335	
Val	Val	Asp	Gly	Arg	Gln	Thr	Gly	Phe	Phe	Thr	Phe	Met	Asp	Ser	Ser
		340							345				350		
Ala	Thr	Tyr	Lys	Ile	Ser	Thr	Lys	Leu	Gly	Ser	Ser	Asn	Asp	Val	Asn
		355					360						365		
Ile	Gln	Glu	Ile	Thr	Gln	Gly	Ala	Lys	Ile	Thr	Pro	Val	Ser	Gly	Glu
	370					375					380				
Lys	Thr	Leu	Pro	Lys	Lys	Phe	Thr	Leu	Lys	Leu	His	Ala	His	Arg	Ser
	385				390					395				400	
Ser	Ser	Thr	Val	Pro	Gly	Thr	Tyr	Thr	Val	Gly	Leu	Asn	Val	Thr	Ser
			405						410					415	
Asn	Val	Ile	Asp	Asn	Lys	Gln	Ala	Ala	Gly	Pro	Thr	Leu	Thr	Lys	Glu
		420							425					430	
Leu	Ala	Leu	Asn	Val	Leu	Ser	Pro	Ala	Ala	Leu	Asp	Ala	Thr	Trp	Ala
		435					440						445		
Pro	Gln	Asp	Asn	Leu	Thr	Leu	Ser	Asn	Thr	Gly	Val	Ser	Asn	Thr	Leu
	450					455					460				
Val	Gly	Val	Leu	Thr	Leu	Ser	Asn	Thr	Ser	Ile	Asp	Thr	Val	Ser	Ile
	465				470					475				480	
Ala	Ser	Thr	Asn	Val	Ser	Asp	Thr	Ser	Lys	Asn	Gly	Thr	Val	Thr	Phe
			485						490					495	
Ala	His	Glu	Thr	Asn	Asn	Ser	Ala	Ser	Phe	Ala	Thr	Thr	Ile	Ser	Thr
			500						505				510		
Asp	Asn	Ala	Asn	Ile	Thr	Leu	Asp	Lys	Asn	Ala	Gly	Asn	Thr	Ile	Val
		515					520						525		
Lys	Thr	Thr	Asn	Gly	Ser	Gln	Leu	Pro	Thr	Asn	Leu	Pro	Leu	Lys	Phe
	530					535					540				
Ile	Thr	Thr	Glu	Gly	Asn	Glu	His	Leu	Val	Ser	Gly	Asn	Tyr	Arg	Ala
	545				550					555				560	
Asn	Ile	Thr	Ile	Thr	Ser	Thr	Ile	Lys	Asp	Asn	Lys	Gln	Ala	Ala	Gly
			565						570					575	
Pro	Thr	Leu	Thr	Lys	Glu	Leu	Ala	Leu	Asn	Val	Leu	Ser	Leu	Glu	His
			580						585					590	
His	His	His	His												
			595												

<210> SEQ ID NO 36  
 <211> LENGTH: 1104  
 <212> TYPE: DNA  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 36

atgaaatacc tgctgccgac cgctgctgct ggtctgctgc tcctogctgc ccagccggcg 60

atggccatgg cagtgggccc aacgaaagat atgagtttag gtgcaaattt aacttcagag 120

cctacattag ctattgattt tacgcctatt gaaaatattt atgtaggctc caattatggt 180

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aaagatattg gaacccttgt ttccacaaca aatgatttaa cagatattac attgatgtca 240
tctcgcagcg ttgttgatgg tcgccagact ggttttttta ccttcacatga ctcacagcc 300
acttacaaaa ttagtacaaa actgggatca tcgaatgatg taaacattca agaaattact 360
caaggagcta aaattactcc tgtagtgga gagaaaactt tgcctaaaaa attcactctt 420
aagctacatg cacacaggag tagcagtaca gttccaggtg cgtatactgt tggcttctaac 480
gtaaccagta acgttattga taacaagcag gcagcggggc ccaactctaac caaagaactg 540
gcattaaatg tgctttctcc tgcagctctg gatgcaactt gggctcctca ggataattta 600
acattatcca atactggcgt ttctaatact ttggtgggtg ttttgactct ttcaaatacc 660
agtattgata cagttagcat tgcgagtaca aatgtttctg atacatctaa gaatggtaca 720
gtaacttttg cacatgagac aaataactct gctagctttg ccaccacat ttcaacagat 780
aatgccaaca ttacgttggg taaaaatgct ggaaatacga ttgttaaaac tacaaatggg 840
agtcagttgc caactaattt accacttaag tttattacca ctgaaggtaa cgaacattta 900
gtttcaggta attaccgtgc aaataaaca attacttcca caattaaaga taacaagcag 960
gcggcaggtc caaccctgac taaggagtta gcgctgaacg ttctatcgat acttgacgaa 1020
taccaatcta aagttaaag acaaatattt tcaggctatc aatctgatat tgatacacat 1080
aatagaatta aggatgaatt atga 1104

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&lt;210&gt; SEQ ID NO 37

&lt;211&gt; LENGTH: 367

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Escherichia coli

&lt;400&gt; SEQUENCE: 37

```

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
1           5           10          15
Ala Gln Pro Ala Met Ala Met Ala Val Gly Pro Thr Lys Asp Met Ser
20          25          30
Leu Gly Ala Asn Leu Thr Ser Glu Pro Thr Leu Ala Ile Asp Phe Thr
35          40          45
Pro Ile Glu Asn Ile Tyr Val Gly Ala Asn Tyr Gly Lys Asp Ile Gly
50          55          60
Thr Leu Val Phe Thr Thr Asn Asp Leu Thr Asp Ile Thr Leu Met Ser
65          70          75          80
Ser Arg Ser Val Val Asp Gly Arg Gln Thr Gly Phe Phe Thr Phe Met
85          90          95
Asp Ser Ser Ala Thr Tyr Lys Ile Ser Thr Lys Leu Gly Ser Ser Asn
100         105         110
Asp Val Asn Ile Gln Glu Ile Thr Gln Gly Ala Lys Ile Thr Pro Val
115         120         125
Ser Gly Glu Lys Thr Leu Pro Lys Lys Phe Thr Leu Lys Leu His Ala
130         135         140
His Arg Ser Ser Ser Thr Val Pro Gly Thr Tyr Thr Val Gly Leu Asn
145         150         155         160
Val Thr Ser Asn Val Ile Asp Asn Lys Gln Ala Ala Gly Pro Thr Leu
165         170         175
Thr Lys Glu Leu Ala Leu Asn Val Leu Ser Pro Ala Ala Leu Asp Ala
180         185         190
Thr Trp Ala Pro Gln Asp Asn Leu Thr Leu Ser Asn Thr Gly Val Ser
195         200         205

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Asn Thr Leu Val Gly Val Leu Thr Leu Ser Asn Thr Ser Ile Asp Thr  
 210 215 220

Val Ser Ile Ala Ser Thr Asn Val Ser Asp Thr Ser Lys Asn Gly Thr  
 225 230 235 240

Val Thr Phe Ala His Glu Thr Asn Asn Ser Ala Ser Phe Ala Thr Thr  
 245 250 255

Ile Ser Thr Asp Asn Ala Asn Ile Thr Leu Asp Lys Asn Ala Gly Asn  
 260 265 270

Thr Ile Val Lys Thr Thr Asn Gly Ser Gln Leu Pro Thr Asn Leu Pro  
 275 280 285

Leu Lys Phe Ile Thr Thr Glu Gly Asn Glu His Leu Val Ser Gly Asn  
 290 295 300

Tyr Arg Ala Asn Ile Thr Ile Thr Ser Thr Ile Lys Asp Asn Lys Gln  
 305 310 315 320

Ala Ala Gly Pro Thr Leu Thr Lys Glu Leu Ala Leu Asn Val Leu Ser  
 325 330 335

Ile Leu Asp Glu Tyr Gln Ser Lys Val Lys Arg Gln Ile Phe Ser Gly  
 340 345 350

Tyr Gln Ser Asp Ile Asp Thr His Asn Arg Ile Lys Asp Glu Leu  
 355 360 365

<210> SEQ ID NO 38  
 <211> LENGTH: 381  
 <212> TYPE: DNA  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 38

```

atgagcttta agaaaattat caaggcattt gttatcatgg ctgctttggg atctgttcag    60
gogcatgcoq ctccccagtc tattacagaa ctatgttcgg aatatacaca cacacaaata    120
tatacgataa atgacaagat actatcatat acggaatcca tggcaggcaa aagagaaatg    180
gttatcatta catttaagag cggcgcaaca ttccaggctg aagtccccgg cagtcaacat    240
atagactccc aaaaaaaaagc cattgaaagg atgaaggaca cattaagaat cgcatatctg    300
accgagacca aaattgataa attatgtgta tggaataata aaacccccga ttcaattgcg    360
gcaatcagta tggaaaacta a                                     381
    
```

<210> SEQ ID NO 39  
 <211> LENGTH: 126  
 <212> TYPE: PRT  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 39

Met Ser Phe Lys Lys Ile Ile Lys Ala Phe Val Ile Met Ala Ala Leu  
 1 5 10 15

Val Ser Val Gln Ala His Ala Ala Pro Gln Ser Ile Thr Glu Leu Cys  
 20 25 30

Ser Glu Tyr His Asn Thr Gln Ile Tyr Thr Ile Asn Asp Lys Ile Leu  
 35 40 45

Ser Tyr Thr Glu Ser Met Ala Gly Lys Arg Glu Met Val Ile Ile Thr  
 50 55 60

Phe Lys Ser Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser Gln His  
 65 70 75 80

Ile Asp Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg  
 85 90 95

Ile Ala Tyr Leu Thr Glu Thr Lys Ile Asp Lys Leu Cys Val Trp Asn

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	100		105		110	
Asn Lys Thr Pro His Ser Ile Ala Ala Ile Ser Met Glu Asn						
	115		120		125	
<p>&lt;210&gt; SEQ ID NO 40                  &lt;211&gt; LENGTH: 1038                  &lt;212&gt; TYPE: DNA                  &lt;213&gt; ORGANISM: Escherichia coli</p>						
<p>&lt;400&gt; SEQUENCE: 40</p>						
atgaaatacc	tgctgccgac	cgctgctgct	ggtctgctgc	tcctcgctgc	ccagccggcg	60
atggccatgt	caaaaagttt	ttttgcacct	gaaccacgaa	tacagccttc	tttggtgaa	120
aatgttgtaa	aggaaggagc	tttattat	agtgtgaact	taactgttcc	tgaaaatgta	180
tcccaggtaa	cggtctaccc	tgtttatgat	gaagattatg	ggtaggacg	actagtaaat	240
accgctgatg	cttccaatc	aataatctac	cagattgttg	atgagaaagg	gaaaaaatg	300
ttaaagatc	atggtgcaga	ggttacacct	aatcaacaaa	taacttttaa	agcgctgaat	360
tatactagcg	gggaaaaaaaa	aatatctcct	ggaatatata	acgatcaggt	tatggttggt	420
tactacgtca	acgacaataa	acaaggaaac	tggaatata	aatctctgga	tgtaaatgta	480
aatattgagc	aaaat	tttat	tccagatatt	gattccgctg	ttcgtataat	540
tacgattcgg	acccgaaact	ggattcacag	ttatatacgg	ttgagatgac	gatccctgca	600
ggtgtaagcg	cagttaaaat	cgcaccaaca	gatagtctga	catcttctgg	acagcagatc	660
ggaaagctgg	ttaatgtaaa	caatccagat	caaaatata	attattatat	cagaaaggat	720
tctggcgtg	gtaactttat	ggcaggacaa	aaaggatcct	ttcctgtcaa	agagaatacg	780
tcatacacat	tctcagcaat	ttatactggt	ggcgaatacc	ctaatagcgg	atattcgtct	840
ggtacttatg	caggaaat	tactgtatca	ttttacagca	atgacaataa	acaaagaaca	900
gaaatagcga	ctaaaaactt	cccagtatca	acgactatat	cgatacttga	cgaataccaa	960
tctaaagtta	aaagacaaat	at	tttcaggc	tatcaatctg	atattgatac	1020
attaaggatg	aattatga					1038
<p>&lt;210&gt; SEQ ID NO 41                  &lt;211&gt; LENGTH: 347                  &lt;212&gt; TYPE: PRT                  &lt;213&gt; ORGANISM: Escherichia coli</p>						
<p>&lt;400&gt; SEQUENCE: 41</p>						
Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Ala						
1		5		10		15
Ala Gln Pro Ala Met Ala Met Glu Gln Asn Phe Ile Pro Asp Ile Asp						
	20		25		30	
Ser Ala Val Arg Ile Ile Pro Val Asn Tyr Asp Ser Asp Pro Lys Leu						
	35		40		45	
Asn Ser Gln Leu Tyr Thr Val Glu Met Thr Ile Pro Ala Gly Val Ser						
	50		55		60	
Ala Val Lys Ile Val Pro Thr Asp Ser Leu Thr Ser Ser Gly Gln Gln						
65		70		75		80
Ile Gly Lys Leu Val Asn Val Asn Asn Pro Asp Gln Asn Met Asn Tyr						
	85		90		95	
Tyr Ile Arg Lys Asp Ser Gly Ala Gly Lys Phe Met Ala Gly Gln Lys						
	100		105		110	
Gly Ser Phe Ser Val Lys Glu Asn Thr Ser Tyr Thr Phe Ser Ala Ile						

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115			120			125									
Tyr	Thr	Gly	Gly	Glu	Tyr	Pro	Asn	Ser	Gly	Tyr	Ser	Ser	Gly	Thr	Tyr
	130						135						140		
Ala	Gly	His	Leu	Thr	Val	Ser	Phe	Tyr	Ser	Asn	Asp	Asn	Lys	Gln	Arg
	145				150						155				160
Thr	Glu	Ile	Ala	Thr	Lys	Asn	Phe	Pro	Val	Ser	Thr	Thr	Ile	Ser	Lys
				165						170				175	
Ser	Phe	Phe	Ala	Pro	Glu	Pro	Gln	Ile	Gln	Pro	Ser	Phe	Gly	Lys	Asn
				180				185					190		
Val	Gly	Lys	Glu	Gly	Asp	Leu	Leu	Phe	Ser	Val	Ser	Leu	Ile	Val	Pro
		195					200						205		
Glu	Asn	Val	Ser	Gln	Val	Thr	Val	Tyr	Pro	Val	Tyr	Asp	Glu	Asp	Tyr
	210						215				220				
Gly	Leu	Gly	Arg	Leu	Val	Asn	Thr	Ala	Asp	Asp	Ser	Gln	Ser	Ile	Ile
	225				230					235					240
Tyr	Gln	Ile	Val	Asp	Asp	Lys	Gly	Lys	Lys	Met	Leu	Lys	Asp	His	Gly
				245						250				255	
Thr	Glu	Val	Thr	Pro	Asn	Gln	Gln	Ile	Thr	Phe	Lys	Ala	Leu	Asn	Tyr
				260				265						270	
Thr	Ser	Gly	Asp	Lys	Glu	Ile	Pro	Pro	Gly	Ile	Tyr	Asn	Asp	Gln	Val
		275					280						285		
Met	Val	Gly	Tyr	Tyr	Val	Asn	Asp	Asn	Lys	Gln	Gly	Asn	Trp	Gln	Tyr
	290						295				300				
Lys	Ser	Leu	Asp	Val	Asn	Val	Asn	Ile	Glu	Gln	Ser	Ile	Leu	Asp	Glu
	305				310					315					320
Tyr	Gln	Ser	Lys	Val	Lys	Arg	Gln	Ile	Phe	Ser	Gly	Tyr	Gln	Ser	Asp
				325						330					335
Ile	Asp	Thr	His	Asn	Arg	Ile	Lys	Asp	Glu	Leu					
				340				345							

&lt;210&gt; SEQ ID NO 42

&lt;211&gt; LENGTH: 1038

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Escherichia coli

&lt;400&gt; SEQUENCE: 42

```

atgaaataacc tgetgccgac cgetgtgtgt ggtctgtgtc tcctcgctgc ccagccggcg      60
atggccatgt caaaaagttt ttttgcacct gaaccacgaa tacagccttc ttttggtgaa      120
aatgttgtaa aggaaggagc tttattatgt agtgtgaact taactgttcc tgaaaatgta      180
tcccaggtaa cgggtctacc tgtttatgat gaagattatg ggtaggacg actagtaaat      240
accgctgatg cttccaatc aataatctac cagattgttg atgagaaagg gaaaaaatg      300
ttaaagatc atggtgcaga ggttacacct aatcaacaaa taacttttaa agcgctgaat      360
tatactagcg gggaaaaaaaa aatatctcct ggaatatata acgatcaggt tatggttggt      420
tactacgtca acgacaataa acaaggaaac tggcaatata aatctctgga tgtaaatgta      480
aatattgagc aaaattttat tccagatatt gattccgctg ttcgtataat acctgttaat      540
tacgattcgg acccgaaact ggattcacag ttatatacgg ttgagatgac gatccctgca      600
gggtgaagcg cagttaaaat cgcaccaaca gatagtctga catcttctgg acagcagatc      660
ggaaagctgg ttaatgtaaa caatccagat caaaatatga attattatat cagaaaggat      720
tctggcgtcg gtaactttat ggcaggacaa aaaggatcct ttctgtcaa agagaatacg      780
tcatacatat tctcagcaat ttactctggt ggccaatacc ctaatagcgg atattcgtct      840

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ggtacttatg caggaaatgt gactgtatca ttttacagca atgacaataa acaaagaaca   900
gaaatagcga ctaaaaactt cccagtatca acgactatat cgatacttga cgaataccaa   960
tctaaagtta aaagacaaat attttcaggc tatcaatctg atattgatac acataataga  1020
attaaggatg aattatga                                     1038

```

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<210> SEQ ID NO 43
<211> LENGTH: 345
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

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<400> SEQUENCE: 43

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```

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
1           5           10           15
Ala Gln Pro Ala Met Ala Met Ser Lys Ser Phe Phe Ala Pro Glu Pro
20          25          30
Arg Ile Gln Pro Ser Phe Gly Glu Asn Val Gly Lys Glu Gly Ala Leu
35          40          45
Leu Phe Ser Val Asn Leu Thr Val Pro Glu Asn Val Ser Gln Val Thr
50          55          60
Val Tyr Pro Val Tyr Asp Glu Asp Tyr Gly Leu Gly Arg Leu Val Asn
65          70          75          80
Thr Ala Asp Ala Ser Gln Ser Ile Ile Tyr Gln Ile Val Asp Glu Lys
85          90          95
Gly Lys Lys Met Leu Lys Asp His Gly Ala Glu Val Thr Pro Asn Gln
100         105         110
Gln Ile Thr Phe Lys Ala Leu Asn Tyr Thr Ser Gly Glu Lys Lys Ile
115         120         125
Ser Pro Gly Ile Tyr Asn Asp Gln Val Met Val Gly Tyr Tyr Val Asn
130         135         140
Asp Asn Lys Gln Gly Asn Trp Gln Tyr Lys Ser Leu Asp Val Asn Val
145         150         155         160
Asn Ile Glu Gln Asn Phe Ile Pro Asp Ile Asp Ser Ala Val Arg Ile
165         170         175
Ile Pro Val Asn Tyr Asp Ser Asp Pro Lys Leu Asp Ser Gln Leu Tyr
180         185         190
Thr Val Glu Met Thr Ile Pro Ala Gly Val Ser Ala Val Lys Ile Ala
195         200         205
Pro Thr Asp Ser Leu Thr Ser Ser Gly Gln Gln Ile Gly Lys Leu Val
210         215         220
Asn Val Asn Asn Pro Asp Gln Asn Met Asn Tyr Tyr Ile Arg Lys Asp
225         230         235         240
Ser Gly Ala Gly Asn Phe Met Ala Gly Gln Lys Gly Ser Phe Pro Val
245         250         255
Lys Glu Asn Thr Ser Tyr Thr Phe Ser Ala Ile Tyr Thr Gly Gly Glu
260         265         270
Tyr Pro Asn Ser Gly Tyr Ser Ser Gly Thr Tyr Ala Gly Asn Leu Thr
275         280         285
Val Ser Phe Tyr Ser Asn Asp Asn Lys Gln Arg Thr Glu Ile Ala Thr
290         295         300
Lys Asn Phe Pro Val Ser Thr Thr Ile Ser Ile Leu Asp Glu Tyr Gln
305         310         315         320
Ser Lys Val Lys Arg Gln Ile Phe Ser Gly Tyr Gln Ser Asp Ile Asp
325         330         335

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-continued

Thr His Asn Arg Ile Lys Asp Glu Leu  
 340 345

<210> SEQ ID NO 44  
 <211> LENGTH: 1092  
 <212> TYPE: DNA  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 44

```

atgaaaaaga tatttatttt ttgtctatc atattttctg cgggtggtcag tgccggggcga    60
taccgcgaaa ctacagtagg taactctgacg aagagttttc aagcccctcg tcaggataga    120
agcgtacaat caccaatata taacatcttt acgaatcatg tggtctggata tagtttgagt    180
cataacttat atgacaggat tgttttttta tgtacatcct cgtcgaatcc ggttaatggt    240
gcttgcccaa ccattggaac atctggagtt caatacggta ctacaacat aaccttgagc    300
tttacagaaa aaagaagtct gataaaaaga aatattaatc ttgcaggtaa taagaaacca    360
atatgggaga atcagagttg cgacactagc aatctaattg tgttgaattc gaagtcttgg    420
tcctgtgggg cttacggaaa tgctaacgga acacttctaa atctgtatat ccctgcagga    480
gaaatcaaca aattgccttt tggagggata tgggaggcaa ctctgatctt acgcttatca    540
agatatggcg aagtcagtag cacccattac ggcaattata ccgtaaatat tacggttgat    600
ttaactgata aaggaatat tcaggtatgg cttccagggt ttcacagcaa cccgcgtgta    660
gacctgaatc tgcaccctat cgtaattat aaatatagtg gtagtaattc actcgacatg    720
tgtttctatg atggatatag tacaacagc gatagcatgg taataaagtt ccaggatgat    780
aatcctacct attcatctga atataatctt tataagatag ggggcaactga aaaattacca    840
tatgtgtttt cactgcttat gggagaaaaa atattttatc cagtgaatgg tcaatcattt    900
actatcaatg acagtagtgt actcgaaca aactggaatc gagtaaccgc agttgctatg    960
ccggaagtta atgttccagt attatgctgg ccagcaagat tgctattaaa tgctgatgta   1020
aatgtcccg atgcaggaca gtattcagga cagatatata taacatttac acccagtgtc   1080
gaaaatttat ga                                     1092
    
```

<210> SEQ ID NO 45  
 <211> LENGTH: 363  
 <212> TYPE: PRT  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 45

```

Met Lys Lys Ile Phe Ile Phe Leu Ser Ile Ile Phe Ser Ala Val Val
 1           5           10          15
Ser Ala Gly Arg Tyr Pro Glu Thr Thr Val Gly Asn Leu Thr Lys Ser
 20          25          30
Phe Gln Ala Pro Arg Gln Asp Arg Ser Val Gln Ser Pro Ile Tyr Asn
 35          40          45
Ile Phe Thr Asn His Val Ala Gly Tyr Ser Leu Ser His Asn Leu Tyr
 50          55          60
Asp Arg Ile Val Phe Leu Cys Thr Ser Ser Ser Asn Pro Val Asn Gly
 65          70          75          80
Ala Cys Pro Thr Ile Gly Thr Ser Gly Val Gln Tyr Gly Thr Thr Thr
 85          90          95
Ile Thr Leu Gln Phe Thr Glu Lys Arg Ser Leu Ile Lys Arg Asn Ile
 100         105         110
    
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Asn Leu Ala Gly Asn Lys Lys Pro Ile Trp Glu Asn Gln Ser Cys Asp  
 115 120 125  
 Thr Ser Asn Leu Met Val Leu Asn Ser Lys Ser Trp Ser Cys Gly Ala  
 130 135 140  
 Tyr Gly Asn Ala Asn Gly Thr Leu Leu Asn Leu Tyr Ile Pro Ala Gly  
 145 150 155 160  
 Glu Ile Asn Lys Leu Pro Phe Gly Gly Ile Trp Glu Ala Thr Leu Ile  
 165 170 175  
 Leu Arg Leu Ser Arg Tyr Gly Glu Val Ser Ser Thr His Tyr Gly Asn  
 180 185 190  
 Tyr Thr Val Asn Ile Thr Val Asp Leu Thr Asp Lys Gly Asn Ile Gln  
 195 200 205  
 Val Trp Leu Pro Gly Phe His Ser Asn Pro Arg Val Asp Leu Asn Leu  
 210 215 220  
 His Pro Ile Gly Asn Tyr Lys Tyr Ser Gly Ser Asn Ser Leu Asp Met  
 225 230 235 240  
 Cys Phe Tyr Asp Gly Tyr Ser Thr Asn Ser Asp Ser Met Val Ile Lys  
 245 250 255  
 Phe Gln Asp Asp Asn Pro Thr Tyr Ser Ser Glu Tyr Asn Leu Tyr Lys  
 260 265 270  
 Ile Gly Gly Thr Glu Lys Leu Pro Tyr Ala Val Ser Leu Leu Met Gly  
 275 280 285  
 Glu Lys Ile Phe Tyr Pro Val Asn Gly Gln Ser Phe Thr Ile Asn Asp  
 290 295 300  
 Ser Ser Val Leu Glu Thr Asn Trp Asn Arg Val Thr Ala Val Ala Met  
 305 310 315 320  
 Pro Glu Val Asn Val Pro Val Leu Cys Trp Pro Ala Arg Leu Leu Leu  
 325 330 335  
 Asn Ala Asp Val Asn Ala Pro Asp Ala Gly Gln Tyr Ser Gly Gln Ile  
 340 345 350  
 Tyr Ile Thr Phe Thr Pro Ser Val Glu Asn Leu  
 355 360

<210> SEQ ID NO 46  
 <211> LENGTH: 345  
 <212> TYPE: PRT  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 46

Gly Arg Tyr Pro Glu Thr Thr Val Gly Asn Leu Thr Lys Ser Phe Gln  
 1 5 10 15  
 Ala Pro Arg Gln Asp Arg Ser Val Gln Ser Pro Ile Tyr Asn Ile Phe  
 20 25 30  
 Thr Asn His Val Ala Gly Tyr Ser Leu Ser His Asn Leu Tyr Asp Arg  
 35 40 45  
 Ile Val Phe Leu Cys Thr Ser Ser Ser Asn Pro Val Asn Gly Ala Cys  
 50 55 60  
 Pro Thr Ile Gly Thr Ser Gly Val Gln Tyr Gly Thr Thr Thr Ile Thr  
 65 70 75 80  
 Leu Gln Phe Thr Glu Lys Arg Ser Leu Ile Lys Arg Asn Ile Asn Leu  
 85 90 95  
 Ala Gly Asn Lys Lys Pro Ile Trp Glu Asn Gln Ser Cys Asp Thr Ser  
 100 105 110  
 Asn Leu Met Val Leu Asn Ser Lys Ser Trp Ser Cys Gly Ala Tyr Gly  
 115 120 125

-continued

Asn Ala Asn Gly Thr Leu Leu Asn Leu Tyr Ile Pro Ala Gly Glu Ile  
 130 135 140

Asn Lys Leu Pro Phe Gly Gly Ile Trp Glu Ala Thr Leu Ile Leu Arg  
 145 150 155 160

Leu Ser Arg Tyr Gly Glu Val Ser Ser Thr His Tyr Gly Asn Tyr Thr  
 165 170 175

Val Asn Ile Thr Val Asp Leu Thr Asp Lys Gly Asn Ile Gln Val Trp  
 180 185 190

Leu Pro Gly Phe His Ser Asn Pro Arg Val Asp Leu Asn Leu His Pro  
 195 200 205

Ile Gly Asn Tyr Lys Tyr Ser Gly Ser Asn Ser Leu Asp Met Cys Phe  
 210 215 220

Tyr Asp Gly Tyr Ser Thr Asn Ser Asp Ser Met Val Ile Lys Phe Gln  
 225 230 235 240

Asp Asp Asn Pro Thr Tyr Ser Ser Glu Tyr Asn Leu Tyr Lys Ile Gly  
 245 250 255

Gly Thr Glu Lys Leu Pro Tyr Ala Val Ser Leu Leu Met Gly Glu Lys  
 260 265 270

Ile Phe Tyr Pro Val Asn Gly Gln Ser Phe Thr Ile Asn Asp Ser Ser  
 275 280 285

Val Leu Glu Thr Asn Trp Asn Arg Val Thr Ala Val Ala Met Pro Glu  
 290 295 300

Val Asn Val Pro Val Leu Cys Trp Pro Ala Arg Leu Leu Leu Asn Ala  
 305 310 315 320

Asp Val Asn Ala Pro Asp Ala Gly Gln Tyr Ser Gly Gln Ile Tyr Ile  
 325 330 335

Thr Phe Thr Pro Ser Val Glu Asn Leu  
 340 345

<210> SEQ ID NO 47  
 <211> LENGTH: 507  
 <212> TYPE: DNA  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 47

atgaaactga agaaaacaat tggcgcaatg gctatggcga ctctgtttgc caccatggct 60  
 gcctctgcag tcgaaaaaaa tattactgtg agggcaatg ttgaccctaa acttgatctt 120  
 ctgcaagcag atggaacttc actgccggac tctatcgcat taacctattc ttcggcttca 180  
 aataattttg aagtttactc tcttaatact gctattcata caaatgacaa aagcaagggg 240  
 gttgtagtga agctgtcagc ttcaccagtt ctgtccaata ttatgaagcc aaactcgcaa 300  
 attccgatga aagtgacttt gggggggaag acgctgaata caactgatac tgagtttact 360  
 gttgatactc tgaactttgg tacatctggt gttgaaaacg tttcttccac tcaacagctt 420  
 acgattcatg cagacacaca aggaactgcg cctgaggcag gcaattacca aggtattatt 480  
 tctcttatca tgactcaaaa aacttaa 507

<210> SEQ ID NO 48  
 <211> LENGTH: 168  
 <212> TYPE: PRT  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 48

Met Lys Leu Lys Lys Thr Ile Gly Ala Met Ala Met Ala Thr Leu Phe  
 1 5 10 15

-continued

Ala Thr Met Ala Ala Ser Ala Val Glu Lys Asn Ile Thr Val Arg Ala  
 20 25 30  
 Ser Val Asp Pro Lys Leu Asp Leu Leu Gln Ala Asp Gly Thr Ser Leu  
 35 40 45  
 Pro Asp Ser Ile Ala Leu Thr Tyr Ser Ser Ala Ser Asn Asn Phe Glu  
 50 55 60  
 Val Tyr Ser Leu Asn Thr Ala Ile His Thr Asn Asp Lys Ser Lys Gly  
 65 70 75 80  
 Val Val Val Lys Leu Ser Ala Ser Pro Val Leu Ser Asn Ile Met Lys  
 85 90 95  
 Pro Asn Ser Gln Ile Pro Met Lys Val Thr Leu Gly Gly Lys Thr Leu  
 100 105 110  
 Asn Thr Thr Asp Thr Glu Phe Thr Val Asp Thr Leu Asn Phe Gly Thr  
 115 120 125  
 Ser Gly Val Glu Asn Val Ser Ser Thr Gln Gln Leu Thr Ile His Ala  
 130 135 140  
 Asp Thr Gln Gly Thr Ala Pro Glu Ala Gly Asn Tyr Gln Gly Ile Ile  
 145 150 155 160  
 Ser Leu Ile Met Thr Gln Lys Thr  
 165

<210> SEQ ID NO 49  
 <211> LENGTH: 145  
 <212> TYPE: PRT  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 49

Val Glu Lys Asn Ile Thr Val Arg Ala Ser Val Asp Pro Lys Leu Asp  
 1 5 10 15  
 Leu Leu Gln Ala Asp Gly Thr Ser Leu Pro Asp Ser Ile Ala Leu Thr  
 20 25 30  
 Tyr Ser Ser Ala Ser Asn Asn Phe Glu Val Tyr Ser Leu Asn Thr Ala  
 35 40 45  
 Ile His Thr Asn Asp Lys Ser Lys Gly Val Val Val Lys Leu Ser Ala  
 50 55 60  
 Ser Pro Val Leu Ser Asn Ile Met Lys Pro Asn Ser Gln Ile Pro Met  
 65 70 75 80  
 Lys Val Thr Leu Gly Gly Lys Thr Leu Asn Thr Thr Asp Thr Glu Phe  
 85 90 95  
 Thr Val Asp Thr Leu Asn Phe Gly Thr Ser Gly Val Glu Asn Val Ser  
 100 105 110  
 Ser Thr Gln Gln Leu Thr Ile His Ala Asp Thr Gln Gly Thr Ala Pro  
 115 120 125  
 Glu Ala Gly Asn Tyr Gln Gly Ile Ile Ser Leu Ile Met Thr Gln Lys  
 130 135 140  
 Thr  
 145

<210> SEQ ID NO 50  
 <211> LENGTH: 1095  
 <212> TYPE: DNA  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 50

ttgaaaaaag tgatttttgt tttatccatg tttctatggt ctcagggtta cgggcaatca 60

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tggcatacga acgtagaggc tggttcaata aataaaacag agtcgatagg ccccatagac 120
cgaagtgctg ctgcatcgta tctgtctcat tatatatttc atgaacatgt tgctgggttac 180
aataaagatc actctctttt tgacaggatg acgtttttat gtatgtcatc aacagatgca 240
tctaaaggtg catgtccgac aggagaaaaac tccaaatcct ctcaagggga gactaatatt 300
aagctaatat ttactgaaaa gaaaagtctg gccagaaaaa cattaacctt aaaaggatat 360
aagagatttt tatatgaatc agatagatgc attcattatg tcgataaaat gaatctcaat 420
tctcatactg ttaaagtgtg aggttcattc acaagaggag tagatttcac tttatatatc 480
ccacaagggtg aaattgatgg gcttctaact ggaggtatat gggaggcaac actagagtta 540
cgagtcaaaa ggcattacga ctataatcat ggtacttaca aagttaatat cacagttgat 600
ttgacagaca aaggaaatat tcaggtctgg acaccaaagt ttcatagcga tcctagaatt 660
gatctgaatt tacgtctcga aggtaatggt aaatattctg gtagtaacgt gcttgagatg 720
tgtctctatg atggctatag tacacatagt caaagtatag aaatgaggtt tcaggatgac 780
tcacaaacag gaaataatga atataatctt ataaaaactg gagagccatt aaaaaaattg 840
ccatataaac tttctcttct tttaggagga cgagagtttt atccaaataa tggagaggct 900
tttactatta atgatacttc gtcattgttt ataaactgga atcgtattaa gtctgtatcc 960
ttaccacaga ttagtattcc agtactatgc tggccagcaa acttgacatt tatgtcagag 1020
ctaaataatc cagaagcggg tgagtattca ggaataacta acgtaacatt tactcctagt 1080
agttcaagtc tgtaa 1095

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<210> SEQ ID NO 51
<211> LENGTH: 364
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

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<400> SEQUENCE: 51

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```

Leu Lys Lys Val Ile Phe Val Leu Ser Met Phe Leu Cys Ser Gln Val
1           5           10           15
Tyr Gly Gln Ser Trp His Thr Asn Val Glu Ala Gly Ser Ile Asn Lys
20          25          30
Thr Glu Ser Ile Gly Pro Ile Asp Arg Ser Ala Ala Ala Ser Tyr Pro
35          40          45
Ala His Tyr Ile Phe His Glu His Val Ala Gly Tyr Asn Lys Asp His
50          55          60
Ser Leu Phe Asp Arg Met Thr Phe Leu Cys Met Ser Ser Thr Asp Ala
65          70          75          80
Ser Lys Gly Ala Cys Pro Thr Gly Glu Asn Ser Lys Ser Ser Gln Gly
85          90          95
Glu Thr Asn Ile Lys Leu Ile Phe Thr Glu Lys Lys Ser Leu Ala Arg
100         105         110
Lys Thr Leu Asn Leu Lys Gly Tyr Lys Arg Phe Leu Tyr Glu Ser Asp
115         120         125
Arg Cys Ile His Tyr Val Asp Lys Met Asn Leu Asn Ser His Thr Val
130         135         140
Lys Cys Val Gly Ser Phe Thr Arg Gly Val Asp Phe Thr Leu Tyr Ile
145         150         155         160
Pro Gln Gly Glu Ile Asp Gly Leu Leu Thr Gly Gly Ile Trp Glu Ala
165         170         175
Thr Leu Glu Leu Arg Val Lys Arg His Tyr Asp Tyr Asn His Gly Thr
180         185         190

```

-continued

Tyr Lys Val Asn Ile Thr Val Asp Leu Thr Asp Lys Gly Asn Ile Gln  
 195 200 205  
 Val Trp Thr Pro Lys Phe His Ser Asp Pro Arg Ile Asp Leu Asn Leu  
 210 215 220  
 Arg Pro Glu Gly Asn Gly Lys Tyr Ser Gly Ser Asn Val Leu Glu Met  
 225 230 235 240  
 Cys Leu Tyr Asp Gly Tyr Ser Thr His Ser Gln Ser Ile Glu Met Arg  
 245 250 255  
 Phe Gln Asp Asp Ser Gln Thr Gly Asn Asn Glu Tyr Asn Leu Ile Lys  
 260 265 270  
 Thr Gly Glu Pro Leu Lys Lys Leu Pro Tyr Lys Leu Ser Leu Leu Leu  
 275 280 285  
 Gly Gly Arg Glu Phe Tyr Pro Asn Asn Gly Glu Ala Phe Thr Ile Asn  
 290 295 300  
 Asp Thr Ser Ser Leu Phe Ile Asn Trp Asn Arg Ile Lys Ser Val Ser  
 305 310 315 320  
 Leu Pro Gln Ile Ser Ile Pro Val Leu Cys Trp Pro Ala Asn Leu Thr  
 325 330 335  
 Phe Met Ser Glu Leu Asn Asn Pro Glu Ala Gly Glu Tyr Ser Gly Ile  
 340 345 350  
 Leu Asn Val Thr Phe Thr Pro Ser Ser Ser Ser Leu  
 355 360

<210> SEQ ID NO 52  
 <211> LENGTH: 346  
 <212> TYPE: PRT  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 52

Gln Ser Trp His Thr Asn Val Glu Ala Gly Ser Ile Asn Lys Thr Glu  
 1 5 10 15  
 Ser Ile Gly Pro Ile Asp Arg Ser Ala Ala Ala Ser Tyr Pro Ala His  
 20 25 30  
 Tyr Ile Phe His Glu His Val Ala Gly Tyr Asn Lys Asp His Ser Leu  
 35 40 45  
 Phe Asp Arg Met Thr Phe Leu Cys Met Ser Ser Thr Asp Ala Ser Lys  
 50 55 60  
 Gly Ala Cys Pro Thr Gly Glu Asn Ser Lys Ser Ser Gln Gly Glu Thr  
 65 70 75 80  
 Asn Ile Lys Leu Ile Phe Thr Glu Lys Lys Ser Leu Ala Arg Lys Thr  
 85 90 95  
 Leu Asn Leu Lys Gly Tyr Lys Arg Phe Leu Tyr Glu Ser Asp Arg Cys  
 100 105 110  
 Ile His Tyr Val Asp Lys Met Asn Leu Asn Ser His Thr Val Lys Cys  
 115 120 125  
 Val Gly Ser Phe Thr Arg Gly Val Asp Phe Thr Leu Tyr Ile Pro Gln  
 130 135 140  
 Gly Glu Ile Asp Gly Leu Thr Gly Gly Ile Trp Glu Ala Thr Leu  
 145 150 155 160  
 Glu Leu Arg Val Lys Arg His Tyr Asp Tyr Asn His Gly Thr Tyr Lys  
 165 170 175  
 Val Asn Ile Thr Val Asp Leu Thr Asp Lys Gly Asn Ile Gln Val Trp  
 180 185 190  
 Thr Pro Lys Phe His Ser Asp Pro Arg Ile Asp Leu Asn Leu Arg Pro

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195					200					205					
Glu	Gly	Asn	Gly	Lys	Tyr	Ser	Gly	Ser	Asn	Val	Leu	Glu	Met	Cys	Leu
210						215					220				
Tyr	Asp	Gly	Tyr	Ser	Thr	His	Ser	Gln	Ser	Ile	Glu	Met	Arg	Phe	Gln
225					230					235					240
Asp	Asp	Ser	Gln	Thr	Gly	Asn	Asn	Glu	Tyr	Asn	Leu	Ile	Lys	Thr	Gly
				245					250					255	
Glu	Pro	Leu	Lys	Lys	Leu	Pro	Tyr	Lys	Leu	Ser	Leu	Leu	Leu	Gly	Gly
			260					265						270	
Arg	Glu	Phe	Tyr	Pro	Asn	Asn	Gly	Glu	Ala	Phe	Thr	Ile	Asn	Asp	Thr
			275				280						285		
Ser	Ser	Leu	Phe	Ile	Asn	Trp	Asn	Arg	Ile	Lys	Ser	Val	Ser	Leu	Pro
290					295					300					
Gln	Ile	Ser	Ile	Pro	Val	Leu	Cys	Trp	Pro	Ala	Asn	Leu	Thr	Phe	Met
305					310					315					320
Ser	Glu	Leu	Asn	Asn	Pro	Glu	Ala	Gly	Glu	Tyr	Ser	Gly	Ile	Leu	Asn
				325					330					335	
Val	Thr	Phe	Thr	Pro	Ser	Ser	Ser	Ser	Leu						
			340					345							

<210> SEQ ID NO 53  
 <211> LENGTH: 513  
 <212> TYPE: DNA  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 53

```

atgaaactca ataagattat tggagcatta gttctttcat ctacatttgt tagcatgggg      60
gcttctgctg ccgagaaaaa tatcactgta actgctagcg ttgatccaac tatcgatctg     120
atgcaatctg atggcacagc gttaccaagt gcagttaata ttgcatatct tccaggagag     180
aaaagatttg aatctgctcg tatcaatacc caagttcata ccaataataa aactaagggt     240
attcagataa agcttactaa tgataatgtg gtaatgacta acttatctga tccaagcaag     300
actattcctt tagaggtttc attcgctggc actaagctga gcacagctgc aacatctatt     360
actgccgatac aattaaattt tggcgcagct ggtgtagaga cagtttctgc aactaaggaa     420
ctcgttatta atgcaggaag caccagcaa actaatattg tagctggtaa ctatcaagga     480
ttggtgtcaa ttgtgcttac tcaagaacct taa                                     513
    
```

<210> SEQ ID NO 54  
 <211> LENGTH: 170  
 <212> TYPE: PRT  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 54

Met	Lys	Leu	Asn	Lys	Ile	Ile	Gly	Ala	Leu	Val	Leu	Ser	Ser	Thr	Phe
1				5					10					15	
Val	Ser	Met	Gly	Ala	Ser	Ala	Ala	Glu	Lys	Asn	Ile	Thr	Val	Thr	Ala
			20					25					30		
Ser	Val	Asp	Pro	Thr	Ile	Asp	Leu	Met	Gln	Ser	Asp	Gly	Thr	Ala	Leu
		35					40					45			
Pro	Ser	Ala	Val	Asn	Ile	Ala	Tyr	Leu	Pro	Gly	Glu	Lys	Arg	Phe	Glu
		50			55						60				
Ser	Ala	Arg	Ile	Asn	Thr	Gln	Val	His	Thr	Asn	Asn	Lys	Thr	Lys	Gly
65				70							75				80
Ile	Gln	Ile	Lys	Leu	Thr	Asn	Asp	Asn	Val	Val	Met	Thr	Asn	Leu	Ser

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	85		90		95										
Asp	Pro	Ser	Lys	Thr	Ile	Pro	Leu	Glu	Val	Ser	Phe	Ala	Gly	Thr	Lys
			100					105					110		
Leu	Ser	Thr	Ala	Ala	Thr	Ser	Ile	Thr	Ala	Asp	Gln	Leu	Asn	Phe	Gly
		115					120					125			
Ala	Ala	Gly	Val	Glu	Thr	Val	Ser	Ala	Thr	Lys	Glu	Leu	Val	Ile	Asn
		130					135				140				
Ala	Gly	Ser	Thr	Gln	Gln	Thr	Asn	Ile	Val	Ala	Gly	Asn	Tyr	Gln	Gly
		145			150					155					160
Leu	Val	Ser	Ile	Val	Leu	Thr	Gln	Glu	Pro						
				165					170						

<210> SEQ ID NO 55  
 <211> LENGTH: 147  
 <212> TYPE: PRT  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 55

Ala	Glu	Lys	Asn	Ile	Thr	Val	Thr	Ala	Ser	Val	Asp	Pro	Thr	Ile	Asp
1				5					10					15	
Leu	Met	Gln	Ser	Asp	Gly	Thr	Ala	Leu	Pro	Ser	Ala	Val	Asn	Ile	Ala
			20					25					30		
Tyr	Leu	Pro	Gly	Glu	Lys	Arg	Phe	Glu	Ser	Ala	Arg	Ile	Asn	Thr	Gln
		35					40					45			
Val	His	Thr	Asn	Asn	Lys	Thr	Lys	Gly	Ile	Gln	Ile	Lys	Leu	Thr	Asn
	50					55					60				
Asp	Asn	Val	Val	Met	Thr	Asn	Leu	Ser	Asp	Pro	Ser	Lys	Thr	Ile	Pro
	65				70					75					80
Leu	Glu	Val	Ser	Phe	Ala	Gly	Thr	Lys	Leu	Ser	Thr	Ala	Ala	Thr	Ser
				85					90					95	
Ile	Thr	Ala	Asp	Gln	Leu	Asn	Phe	Gly	Ala	Ala	Gly	Val	Glu	Thr	Val
			100					105					110		
Ser	Ala	Thr	Lys	Glu	Leu	Val	Ile	Asn	Ala	Gly	Ser	Thr	Gln	Gln	Thr
		115						120					125		
Asn	Ile	Val	Ala	Gly	Asn	Tyr	Gln	Gly	Leu	Val	Ser	Ile	Val	Leu	Thr
		130				135							140		
Gln	Glu	Pro													
145															

<210> SEQ ID NO 56  
 <211> LENGTH: 1083  
 <212> TYPE: DNA  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 56

atgaataaaa	ttttatttat	ttttacattg	tttttttctt	cagggttttt	tacatttgcc	60
gtatcggcag	ataaaaatcc	cggaagtgaa	aacatgacta	atactattgg	tccccatgac	120
agggggggat	cttcccccat	atataatc	ttaaattcct	atcttacagc	atacaatgga	180
agccatcacc	tgtatgatag	gatgagtttt	ttatgtttgt	cttctcaaaa	tacactgaat	240
ggagcatgcc	caagcagtga	tgcccctggc	actgctacaa	ttgatggcga	aacaaatata	300
acattacaat	ttacggaaaa	aagaagtcta	attaaaagag	aactgcaaat	taaaggctat	360
aaacaatttt	tgttcaaaaa	tgctaattgc	ccatctaaac	tagcacttaa	ctcatctcat	420
tttcaatgta	atagagaaca	agcttcaggt	gctactttat	cgttatacat	accagctggt	480

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gaattaaata aattaccttt tgggggggtc tggaatgccg ttctgaagct aaatgtaaaa 540
agacgatatg atacaaccta tgggacttac actataaaca tcacagtaa tttactgat 600
aaggaaata ttcagatag gttaccacag ttcaaaagta acgctcgtgt cgatcttaac 660
ttgctccaa ctggtggtgg tacatatatc ggaagaaatt ctgttgatg gtgctttat 720
gatgatata gtactaacag cagctctttg gagataagat ttcaggatga taattctaaa 780
tctgatggaa aatattatct aaagaaaata aatgatgact ccaagaact tgtatacact 840
ttgtcacttc tcctggcagg taaaaattha acaccaacaa atggacaggc attaaatatt 900
aacactgctt ctctggaac aaactggaat agaattacag ctgtcacat gccagaaatc 960
agtgttccgg tgtgtgtgtg gcttgacgt ttgcaattgg atgcaaaagt gaaaaatccc 1020
gaggctggac aatatatggg gaatattaaa attactttca caccaagtag tcaaacactc 1080
tag 1083

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&lt;210&gt; SEQ ID NO 57

&lt;211&gt; LENGTH: 360

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Escherichia coli

&lt;400&gt; SEQUENCE: 57

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Met Asn Lys Ile Leu Phe Ile Phe Thr Leu Phe Phe Ser Ser Gly Phe
1          5          10          15
Phe Thr Phe Ala Val Ser Ala Asp Lys Asn Pro Gly Ser Glu Asn Met
20          25          30
Thr Asn Thr Ile Gly Pro His Asp Arg Gly Gly Ser Ser Pro Ile Tyr
35          40          45
Asn Ile Leu Asn Ser Tyr Leu Thr Ala Tyr Asn Gly Ser His His Leu
50          55          60
Tyr Asp Arg Met Ser Phe Leu Cys Leu Ser Ser Gln Asn Thr Leu Asn
65          70          75          80
Gly Ala Cys Pro Ser Ser Asp Ala Pro Gly Thr Ala Thr Ile Asp Gly
85          90          95
Glu Thr Asn Ile Thr Leu Gln Phe Thr Glu Lys Arg Ser Leu Ile Lys
100         105         110
Arg Glu Leu Gln Ile Lys Gly Tyr Lys Gln Phe Leu Phe Lys Asn Ala
115         120         125
Asn Cys Pro Ser Lys Leu Ala Leu Asn Ser Ser His Phe Gln Cys Asn
130         135         140
Arg Glu Gln Ala Ser Gly Ala Thr Leu Ser Leu Tyr Ile Pro Ala Gly
145         150         155         160
Glu Leu Asn Lys Leu Pro Phe Gly Gly Val Trp Asn Ala Val Leu Lys
165         170         175
Leu Asn Val Lys Arg Arg Tyr Asp Thr Thr Tyr Gly Thr Tyr Thr Ile
180         185         190
Asn Ile Thr Val Asn Leu Thr Asp Lys Gly Asn Ile Gln Ile Trp Leu
195         200         205
Pro Gln Phe Lys Ser Asn Ala Arg Val Asp Leu Asn Leu Arg Pro Thr
210         215         220
Gly Gly Gly Thr Tyr Ile Gly Arg Asn Ser Val Asp Met Cys Phe Tyr
225         230         235         240
Asp Gly Tyr Ser Thr Asn Ser Ser Ser Leu Glu Ile Arg Phe Gln Asp
245         250         255
Asp Asn Ser Lys Ser Asp Gly Lys Phe Tyr Leu Lys Lys Ile Asn Asp

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Gly Gln Ala Leu Asn Ile Asn Thr Ala Ser Leu Glu Thr Asn Trp Asn  
 275 280 285  
 Arg Ile Thr Ala Val Thr Met Pro Glu Ile Ser Val Pro Val Leu Cys  
 290 295 300  
 Trp Pro Gly Arg Leu Gln Leu Asp Ala Lys Val Lys Asn Pro Glu Ala  
 305 310 315 320  
 Gly Gln Tyr Met Gly Asn Ile Lys Ile Thr Phe Thr Pro Ser Ser Gln  
 325 330 335

Thr Leu

<210> SEQ ID NO 59  
 <211> LENGTH: 513  
 <212> TYPE: DNA  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 59

atgaaattta aaaaaactat tggtgcaatg gctctgacca caatgtttgt agcagtgagt 60  
 gcttcagcag tagagaaaaa tattactgta acagctagtg ttgatcctgc aattgatctt 120  
 ttgcaagctg atggcaatgc tctgccatca gctgtaaagt tagcttattc tccgcatca 180  
 aaaacttttg aaagttacag agtaatgact caagttcata caaacgatgc aactaaaaaa 240  
 gtaattgtta aacttgctga tacaccacag cttacagatg ttctgaattc aactgttcaa 300  
 atgcctatca gtgtgtcatg gggaggacaa gtattateta caacagccaa agaatttgaa 360  
 gctgctgctt tgggatattc tgcacccggt gtaaatggcg tatcatcttc tcaagagtta 420  
 gtaattagcg ctgcacctaa aactgcccgt accgccccaa ctgcaggaaa ctattcagga 480  
 gtagtatctc ttgtaatgac tttgggatcc tga 513

<210> SEQ ID NO 60  
 <211> LENGTH: 170  
 <212> TYPE: PRT  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 60

Met Lys Phe Lys Lys Thr Ile Gly Ala Met Ala Leu Thr Thr Met Phe  
 1 5 10 15  
 Val Ala Val Ser Ala Ser Ala Val Glu Lys Asn Ile Thr Val Thr Ala  
 20 25 30  
 Ser Val Asp Pro Ala Ile Asp Leu Leu Gln Ala Asp Gly Asn Ala Leu  
 35 40 45  
 Pro Ser Ala Val Lys Leu Ala Tyr Ser Pro Ala Ser Lys Thr Phe Glu  
 50 55 60  
 Ser Tyr Arg Val Met Thr Gln Val His Thr Asn Asp Ala Thr Lys Lys  
 65 70 75 80  
 Val Ile Val Lys Leu Ala Asp Thr Pro Gln Leu Thr Asp Val Leu Asn  
 85 90 95  
 Ser Thr Val Gln Met Pro Ile Ser Val Ser Trp Gly Gly Gln Val Leu  
 100 105 110  
 Ser Thr Thr Ala Lys Glu Phe Glu Ala Ala Ala Leu Gly Tyr Ser Ala  
 115 120 125  
 Ser Gly Val Asn Gly Val Ser Ser Ser Gln Glu Leu Val Ile Ser Ala  
 130 135 140  
 Ala Pro Lys Thr Ala Gly Thr Ala Pro Thr Ala Gly Asn Tyr Ser Gly  
 145 150 155 160  
 Val Val Ser Leu Val Met Thr Leu Gly Ser

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165 170

<210> SEQ ID NO 61  
 <211> LENGTH: 147  
 <212> TYPE: PRT  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 61

Val Glu Lys Asn Ile Thr Val Thr Ala Ser Val Asp Pro Ala Ile Asp  
 1 5 10 15  
 Leu Leu Gln Ala Asp Gly Asn Ala Leu Pro Ser Ala Val Lys Leu Ala  
 20 25 30  
 Tyr Ser Pro Ala Ser Lys Thr Phe Glu Ser Tyr Arg Val Met Thr Gln  
 35 40 45  
 Val His Thr Asn Asp Ala Thr Lys Lys Val Ile Val Lys Leu Ala Asp  
 50 55 60  
 Thr Pro Gln Leu Thr Asp Val Leu Asn Ser Thr Val Gln Met Pro Ile  
 65 70 75 80  
 Ser Val Ser Trp Gly Gly Gln Val Leu Ser Thr Thr Ala Lys Glu Phe  
 85 90 95  
 Glu Ala Ala Ala Leu Gly Tyr Ser Ala Ser Gly Val Asn Gly Val Ser  
 100 105 110  
 Ser Ser Gln Glu Leu Val Ile Ser Ala Ala Pro Lys Thr Ala Gly Thr  
 115 120 125  
 Ala Pro Thr Ala Gly Asn Tyr Ser Gly Val Val Ser Leu Val Met Thr  
 130 135 140  
 Leu Gly Ser  
 145

<210> SEQ ID NO 62  
 <211> LENGTH: 504  
 <212> TYPE: DNA  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 62

atgaaattaa aaaaaactat tggtgcaatg gcaactgacca caatgtttgt agctatgagt 60  
 gcttctgcag tagagaaaaa tatcactgta acagctagtg ttgatcctac aattgatatt 120  
 ttgcaagctg atggtagtag tttacctact gctgtagaat taacctattc acctgcggca 180  
 agtcgttttg aaaattataa aatcgcaact aaagttcata caaatgttat aaataaaaat 240  
 gtactagtta agcttgtaaa tgatccaaaa cttacaaaatg ttttgattc tacaaaaaca 300  
 ctccccatta ctgtatcata tggaggaaaag actctatcaa ccgcagatgt gacttttgaa 360  
 cctgcagaat taaattttgg aacgtcaggt gtaactggtg tatcttcttc ccaagattta 420  
 gtgattggtg cgactacagc acaagcacca acggcgggaa attatagtgg ggtcgtttct 480  
 atcttaatga ccttagcatc ataa 504

<210> SEQ ID NO 63  
 <211> LENGTH: 167  
 <212> TYPE: PRT  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 63

Met Lys Leu Lys Lys Thr Ile Gly Ala Met Ala Leu Thr Thr Met Phe  
 1 5 10 15  
 Val Ala Met Ser Ala Ser Ala Val Glu Lys Asn Ile Thr Val Thr Ala  
 20 25 30

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Ser Val Asp Pro Thr Ile Asp Ile Leu Gln Ala Asp Gly Ser Ser Leu  
 35 40 45  
 Pro Thr Ala Val Glu Leu Thr Tyr Ser Pro Ala Ala Ser Arg Phe Glu  
 50 55 60  
 Asn Tyr Lys Ile Ala Thr Lys Val His Thr Asn Val Ile Asn Lys Asn  
 65 70 75 80  
 Val Leu Val Lys Leu Val Asn Asp Pro Lys Leu Thr Asn Val Leu Asp  
 85 90 95  
 Ser Thr Lys Gln Leu Pro Ile Thr Val Ser Tyr Gly Gly Lys Thr Leu  
 100 105 110  
 Ser Thr Ala Asp Val Thr Phe Glu Pro Ala Glu Leu Asn Phe Gly Thr  
 115 120 125  
 Ser Gly Val Thr Gly Val Ser Ser Ser Gln Asp Leu Val Ile Gly Ala  
 130 135 140  
 Thr Thr Ala Gln Ala Pro Thr Ala Gly Asn Tyr Ser Gly Val Val Ser  
 145 150 155 160  
 Ile Leu Met Thr Leu Ala Ser  
 165

<210> SEQ ID NO 64  
 <211> LENGTH: 1086  
 <212> TYPE: DNA  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 64

atgaataaga ttttatttat ttttacattg tttttctctt cagtactttt tacatttgct 60  
 gtatcggcag ataaaattcc cggagatgaa agcataacta atatttttgg cccgcgtgac 120  
 aggaacgaat cttcccccaa acataatata ttaaataacc atattacagc atacagtgaa 180  
 agtcatactc tgtatgatag gatgactttt ttatgtttgt cttctcacia tacacttaat 240  
 ggagcatgtc caaccagtga gaatcctagc agttcctegg tcagcgggtga aacaaatata 300  
 acattacaat ttacggaaaa aagaagtta ataaaaagag agctacaaat taaaggctat 360  
 aaacaattat tgttcaaaag tgtaactgc ccatcgggcc taacacttaa ctgagctcat 420  
 ttaactgta ataaaaacgc ggcttcaggt gcaagtttat atttatatat tcctgctggc 480  
 gaactaaaaa atttgccttt tgggtgtatc tgggatgcta ctctgaagtt aagagtaaaa 540  
 agacgatata gtgagacctt tggaaactac actataaata tcaactataa attaaactgat 600  
 aagggaaata ttcagatgat gttacctcag ttcaaaagtg acgctcgcgt cgatcttaac 660  
 ttgcttccaa ctggtggggg cacatatatt ggaagaaatt ctggtgatat gtgcttttat 720  
 gatggatata gtactaacag cagctctttg gagataagat ttcaggataa caatcctaaa 780  
 tctgatggga aattttatct aaggaaaaata aatgatgaca ccaaagaaat tgcataact 840  
 ttgtcacttc tcttggcggg taaaagtta actccaacaa atggaacgct attaaatatt 900  
 gctgacgcag cttctctgga aacaaactgg aatagaatta cagctgtcac catgccagaa 960  
 atcagtgttc cgggtgtgtg ttggcctgga cgtttgcaat tggatgcaaa agtggaaaaat 1020  
 cccgaggctg gacaatatat gggtaatat aatgttactt tcacaccaag tagtcaaaaca 1080  
 ctctag 1086

<210> SEQ ID NO 65  
 <211> LENGTH: 361  
 <212> TYPE: PRT  
 <213> ORGANISM: Escherichia coli

-continued

&lt;400&gt; SEQUENCE: 65

Met Asn Lys Ile Leu Phe Ile Phe Thr Leu Phe Phe Ser Ser Val Leu  
 1 5 10 15  
 Phe Thr Phe Ala Val Ser Ala Asp Lys Ile Pro Gly Asp Glu Ser Ile  
 20 25 30  
 Thr Asn Ile Phe Gly Pro Arg Asp Arg Asn Glu Ser Ser Pro Lys His  
 35 40 45  
 Asn Ile Leu Asn Asn His Ile Thr Ala Tyr Ser Glu Ser His Thr Leu  
 50 55 60  
 Tyr Asp Arg Met Thr Phe Leu Cys Leu Ser Ser His Asn Thr Leu Asn  
 65 70 75 80  
 Gly Ala Cys Pro Thr Ser Glu Asn Pro Ser Ser Ser Val Ser Gly  
 85 90 95  
 Glu Thr Asn Ile Thr Leu Gln Phe Thr Glu Lys Arg Ser Leu Ile Lys  
 100 105 110  
 Arg Glu Leu Gln Ile Lys Gly Tyr Lys Gln Leu Leu Phe Lys Ser Val  
 115 120 125  
 Asn Cys Pro Ser Gly Leu Thr Leu Asn Ser Ala His Phe Asn Cys Asn  
 130 135 140  
 Lys Asn Ala Ala Ser Gly Ala Ser Leu Tyr Leu Tyr Ile Pro Ala Gly  
 145 150 155 160  
 Glu Leu Lys Asn Leu Pro Phe Gly Gly Ile Trp Asp Ala Thr Leu Lys  
 165 170 175  
 Leu Arg Val Lys Arg Arg Tyr Ser Glu Thr Tyr Gly Thr Tyr Thr Ile  
 180 185 190  
 Asn Ile Thr Ile Lys Leu Thr Asp Lys Gly Asn Ile Gln Ile Trp Leu  
 195 200 205  
 Pro Gln Phe Lys Ser Asp Ala Arg Val Asp Leu Asn Leu Arg Pro Thr  
 210 215 220  
 Gly Gly Gly Thr Tyr Ile Gly Arg Asn Ser Val Asp Met Cys Phe Tyr  
 225 230 235 240  
 Asp Gly Tyr Ser Thr Asn Ser Ser Ser Leu Glu Ile Arg Phe Gln Asp  
 245 250 255  
 Asn Asn Pro Lys Ser Asp Gly Lys Phe Tyr Leu Arg Lys Ile Asn Asp  
 260 265 270  
 Asp Thr Lys Glu Ile Ala Tyr Thr Leu Ser Leu Leu Leu Ala Gly Lys  
 275 280 285  
 Ser Leu Thr Pro Thr Asn Gly Thr Ser Leu Asn Ile Ala Asp Ala Ala  
 290 295 300  
 Ser Leu Glu Thr Asn Trp Asn Arg Ile Thr Ala Val Thr Met Pro Glu  
 305 310 315 320  
 Ile Ser Val Pro Val Leu Cys Trp Pro Gly Arg Leu Gln Leu Asp Ala  
 325 330 335  
 Lys Val Glu Asn Pro Glu Ala Gly Gln Tyr Met Gly Asn Ile Asn Val  
 340 345 350  
 Thr Phe Thr Pro Ser Ser Gln Thr Leu  
 355 360

&lt;210&gt; SEQ ID NO 66

&lt;211&gt; LENGTH: 510

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Escherichia coli

&lt;400&gt; SEQUENCE: 66

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atgaaattaa aaaaaactat tggcgcaatg gctctgagca caatatttgt agcggtgagt      60
gcttcagcag tagagaaaaa tattactgtg acagccagtg ttgatcctac tattgatatt      120
cttcaagcaa atggttctgc gctaccgaca gctgtagatt taacttatct acctggtgca      180
aaaaacttttg aaaattacag tgttctaacc cagatttaca caaatgaccc ttcaaaaggt      240
ttagatgttc gactggttga tacaccgaaa cttacaaata ttttgcaacc gacatctacc      300
attcctctta ctgtctcatg ggcaggaggg acattaagta caagtgtca gaagatcgca      360
gttgcgcatc tgggttttgg ttccaccgga acggcaggtg tttcgaatag taaagaatta      420
gtaattggag caactacatc cggaaactgca ccaagtgcag gtaagtatca aggcgtcggt      480
tccattgtaa tgactcaatc gacaaaactaa      510

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<210> SEQ ID NO 67
<211> LENGTH: 169
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

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<400> SEQUENCE: 67

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Met Lys Leu Lys Lys Thr Ile Gly Ala Met Ala Leu Ser Thr Ile Phe
 1          5          10          15
Val Ala Val Ser Ala Ser Ala Val Glu Lys Asn Ile Thr Val Thr Ala
 20          25          30
Ser Val Asp Pro Thr Ile Asp Ile Leu Gln Ala Asn Gly Ser Ala Leu
 35          40          45
Pro Thr Ala Val Asp Leu Thr Tyr Leu Pro Gly Ala Lys Thr Phe Glu
 50          55          60
Asn Tyr Ser Val Leu Thr Gln Ile Tyr Thr Asn Asp Pro Ser Lys Gly
 65          70          75          80
Leu Asp Val Arg Leu Val Asp Thr Pro Lys Leu Thr Asn Ile Leu Gln
 85          90          95
Pro Thr Ser Thr Ile Pro Leu Thr Val Ser Trp Ala Gly Arg Thr Leu
100          105          110
Ser Thr Ser Ala Gln Lys Ile Ala Val Gly Asp Leu Gly Phe Gly Ser
115          120          125
Thr Gly Thr Ala Gly Val Ser Asn Ser Lys Glu Leu Val Ile Gly Ala
130          135          140
Thr Thr Ser Gly Thr Ala Pro Ser Ala Gly Lys Tyr Gln Gly Val Val
145          150          155          160
Ser Ile Val Met Thr Gln Ser Thr Asn
165

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<210> SEQ ID NO 68
<211> LENGTH: 528
<212> TYPE: DNA
<213> ORGANISM: Escherichia coli

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<400> SEQUENCE: 68

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atgaaattaa aaaaaactat tggcgcaatg gctctgagca caatgtttgt agcggtgagt      60
gcttcagcag tagagaaaaa tattactgtg acagccagtg ttgatcctac tattgatatt      120
cttcaagcaa atggttctgc gctaccgaca gctgtagatt taacttatct acctggtgca      180
aaaaacttttg aaaattacag tgttctaacc cagatttaca caaatgaccc ttcaaaaggt      240
ttagatgttc gactggttga tacaccgaaa cttacaaata ttttgcaacc gacatctacc      300
attcctctta ctgtctcatg ggcagggaag acattaagta caagtgtca gaagattgca      360

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gttgcgatc tgggttttgg ttccaccgga acggcaggtg tttcgaatag taaagaatta 420  
 gtaattggag caactacatc cggaaactgca ccaagtgcag gtaagtatca aggcgctggt 480  
 tccattgtaa tgactcaatc gacagacaca gccgcgcctg ttccttaa 528

<210> SEQ ID NO 69  
 <211> LENGTH: 175  
 <212> TYPE: PRT  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 69

Met Lys Leu Lys Lys Thr Ile Gly Ala Met Ala Leu Ser Thr Met Phe  
 1 5 10 15  
 Val Ala Val Ser Ala Ser Ala Val Glu Lys Asn Ile Thr Val Thr Ala  
 20 25 30  
 Ser Val Asp Pro Thr Ile Asp Ile Leu Gln Ala Asn Gly Ser Ala Leu  
 35 40 45  
 Pro Thr Ala Val Asp Leu Thr Tyr Leu Pro Gly Ala Lys Thr Phe Glu  
 50 55 60  
 Asn Tyr Ser Val Leu Thr Gln Ile Tyr Thr Asn Asp Pro Ser Lys Gly  
 65 70 75 80  
 Leu Asp Val Arg Leu Val Asp Thr Pro Lys Leu Thr Asn Ile Leu Gln  
 85 90 95  
 Pro Thr Ser Thr Ile Pro Leu Thr Val Ser Trp Ala Gly Lys Thr Leu  
 100 105 110  
 Ser Thr Ser Ala Gln Lys Ile Ala Val Gly Asp Leu Gly Phe Gly Ser  
 115 120 125  
 Thr Gly Thr Ala Gly Val Ser Asn Ser Lys Glu Leu Val Ile Gly Ala  
 130 135 140  
 Thr Thr Ser Gly Thr Ala Pro Ser Ala Gly Lys Tyr Gln Gly Val Val  
 145 150 155 160  
 Ser Ile Val Met Thr Gln Ser Thr Asp Thr Ala Ala Pro Val Pro  
 165 170 175

<210> SEQ ID NO 70  
 <211> LENGTH: 1086  
 <212> TYPE: DNA  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 70

atgaataaga ttttatttat ttttacattg tttttctctt cagtactttt tacatttgc 60  
 gtatcggcag ataaaattcc cggagatgag aatataacta atatttttgg cccgcgtgac 120  
 aggaacgaat cttcccccaa acataatata ttaaatgact atattacagc atacagtgaa 180  
 agtcatactc tgtatgatag gatgattttt ttatgtttgt cttctcaaaa tacacttaat 240  
 ggagcatgtc caaccagtga gaatcctagc agttcatcgg tcagtgccga aacaaatata 300  
 acattacaat ttacggaaaa aagaagtta attaaaagag agctacaaat taaaggctat 360  
 aaacgattat tgttcaaagg tgctaactgc ccatcctacc taacacttaa ctcagctcat 420  
 tatacctgca atagaaaactc ggcttcaggt gcaagtttat atttatatat tcctgctggc 480  
 gaactaaaaa atttaccttt tgggtgtatc tgggatgcta ctctgaagtt aagagtaaaa 540  
 agacgatatg atcagaccta tggaacttac actataaata tcaactgtaa attaactgat 600  
 aagggaata ttcagatag gttacctcag ttcaaaagtg acgctcgcgt cgatcttaac 660  
 ttgcgtccaa ctggtggggg cacatatatt ggaagaaatt ctgttgatg gtgcttttat 720

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gatgatata gtactaacag cagctctttg gagctaagat ttcaggataa caatcctaaa    780
tctgatggga aattttatct aaggaaaata aatgatgaca ccaaagaaat tgcataact    840
ttgtcacttc tcttgggcggg taaaagtta actccaacaa atggaacgctc attaaatatt    900
getgacgcag cttctctgga aataaactgg aatagaatta cagctgtcac catgccagaa    960
atcagtgttc cgggtttgtg ttggcctgga cgtttgcaat tggatgcaaa agtggaaaat   1020
cccgagggcgg gacaatatat gggtaaatatt aatattactt tcacaccaag tagtcaaaaca   1080
ctctag                                           1086
    
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<210> SEQ ID NO 71
<211> LENGTH: 361
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli
    
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<400> SEQUENCE: 71

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Met Asn Lys Ile Leu Phe Ile Phe Thr Leu Phe Phe Ser Ser Val Leu
1           5           10          15
Phe Thr Phe Ala Val Ser Ala Asp Lys Ile Pro Gly Asp Glu Asn Ile
20        25        30
Thr Asn Ile Phe Gly Pro Arg Asp Arg Asn Glu Ser Ser Pro Lys His
35        40        45
Asn Ile Leu Asn Asp Tyr Ile Thr Ala Tyr Ser Glu Ser His Thr Leu
50        55        60
Tyr Asp Arg Met Ile Phe Leu Cys Leu Ser Ser Gln Asn Thr Leu Asn
65        70        75        80
Gly Ala Cys Pro Thr Ser Glu Asn Pro Ser Ser Ser Val Ser Gly
85        90        95
Glu Thr Asn Ile Thr Leu Gln Phe Thr Glu Lys Arg Ser Leu Ile Lys
100       105       110
Arg Glu Leu Gln Ile Lys Gly Tyr Lys Arg Leu Leu Phe Lys Gly Ala
115       120       125
Asn Cys Pro Ser Tyr Leu Thr Leu Asn Ser Ala His Tyr Thr Cys Asn
130       135       140
Arg Asn Ser Ala Ser Gly Ala Ser Leu Tyr Leu Tyr Ile Pro Ala Gly
145       150       155       160
Glu Leu Lys Asn Leu Pro Phe Gly Gly Ile Trp Asp Ala Thr Leu Lys
165       170       175
Leu Arg Val Lys Arg Arg Tyr Asp Gln Thr Tyr Gly Thr Tyr Thr Ile
180       185       190
Asn Ile Thr Val Lys Leu Thr Asp Lys Gly Asn Ile Gln Ile Trp Leu
195       200       205
Pro Gln Phe Lys Ser Asp Ala Arg Val Asp Leu Asn Leu Arg Pro Thr
210       215       220
Gly Gly Gly Thr Tyr Ile Gly Arg Asn Ser Val Asp Met Cys Phe Tyr
225       230       235       240
Asp Gly Tyr Ser Thr Asn Ser Ser Ser Leu Glu Leu Arg Phe Gln Asp
245       250       255
Asn Asn Pro Lys Ser Asp Gly Lys Phe Tyr Leu Arg Lys Ile Asn Asp
260       265       270
Asp Thr Lys Glu Ile Ala Tyr Thr Leu Ser Leu Leu Leu Ala Gly Lys
275       280       285
Ser Leu Thr Pro Thr Asn Gly Thr Ser Leu Asn Ile Ala Asp Ala Ala
290       295       300
    
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Ser Leu Glu Ile Asn Trp Asn Arg Ile Thr Ala Val Thr Met Pro Glu  
 305 310 315 320

Ile Ser Val Pro Val Leu Cys Trp Pro Gly Arg Leu Gln Leu Asp Ala  
 325 330 335

Lys Val Glu Asn Pro Glu Ala Gly Gln Tyr Met Gly Asn Ile Asn Ile  
 340 345 350

Thr Phe Thr Pro Ser Ser Gln Thr Leu  
 355 360

<210> SEQ ID NO 72  
 <211> LENGTH: 516  
 <212> TYPE: DNA  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 72

atgaaactaa agaaaacaat tggcgcaatg gctctggcga cattatttgc aactatggga 60  
 gcatctgcgg tcgagaagac cattagcgtt acggcgagtg ttgacccgac tgttgacctt 120  
 ctgcaatctg atggctctgc gctgcccgaac tctgtcgcac taacctattc tccggetgta 180  
 aataattttg aagctcacac catcaacacc gttgttcata caaatgactc agataaaggt 240  
 gttgttga agctgtcagc agatccagtc ctgtccaatg ttctgaatcc aacctgcaa 300  
 attctgttt ctgtgaattt cgcaggaaaa ccaactgagca caacaggeat taccatcgac 360  
 tccaatgatc tgaactttgc ttcgagtggg tttaataaag tttcttctac gcagaaactt 420  
 tcaatccatg cagatgtcac tcgggtaact ggcggcgcac taacagctgg tcaatatcag 480  
 ggactcgtat caattatcct gactaagtca acgtaa 516

<210> SEQ ID NO 73  
 <211> LENGTH: 171  
 <212> TYPE: PRT  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 73

Met Lys Leu Lys Lys Thr Ile Gly Ala Met Ala Leu Ala Thr Leu Phe  
 1 5 10 15

Ala Thr Met Gly Ala Ser Ala Val Glu Lys Thr Ile Ser Val Thr Ala  
 20 25 30

Ser Val Asp Pro Thr Val Asp Leu Leu Gln Ser Asp Gly Ser Ala Leu  
 35 40 45

Pro Asn Ser Val Ala Leu Thr Tyr Ser Pro Ala Val Asn Asn Phe Glu  
 50 55 60

Ala His Thr Ile Asn Thr Val Val His Thr Asn Asp Ser Asp Lys Gly  
 65 70 75 80

Val Val Val Lys Leu Ser Ala Asp Pro Val Leu Ser Asn Val Leu Asn  
 85 90 95

Pro Thr Leu Gln Ile Pro Val Ser Val Asn Phe Ala Gly Lys Pro Leu  
 100 105 110

Ser Thr Thr Gly Ile Thr Ile Asp Ser Asn Asp Leu Asn Phe Ala Ser  
 115 120 125

Ser Gly Val Asn Lys Val Ser Ser Thr Gln Lys Leu Ser Ile His Ala  
 130 135 140

Asp Ala Thr Arg Val Thr Gly Gly Ala Leu Thr Ala Gly Gln Tyr Gln  
 145 150 155 160

Gly Leu Val Ser Ile Ile Leu Thr Lys Ser Thr  
 165 170

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<210> SEQ ID NO 74
<211> LENGTH: 1092
<212> TYPE: DNA
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 74
atgaaaaaga tatttatttt ttgtctatc atattttctg cgggtggtcag tgccgggcca      60
taccocgaaa ctacagtagg taactctgacg aagagttttc aagcccctcg tctggataga      120
agcgtacaat caccaatata taacatcttt acgaatcatg tggtctggata tagtttgagt      180
catagcttat atgacaggat tgttttttta tgtacatcct cgtcgaatcc ggttaatggt      240
gcttgcccaa ccattggaac atctggagtt caatacggta ctacaacat aaccttgagc      300
tttacagaaa aaagaagtct gataaaaaa aatattaatc ttgcaggtaa taagaaacca      360
atatgggaga atcagagttg cgactttagc aatctaattg tgttgaattc gaagtcttgg      420
agctgtgggg cttacggaaa tgctaacgga acacttctaa atctgtatat ccctgcagga      480
gaaatcaaca aattgccttt tggagggata tgggaggcaa ctctgatctt acgcttatca      540
agatatggcg aagtcagtag cacccattac ggcaattata ccgtaaatat tacggttgat      600
ttaactgata aaggaatat tcaggtatgg cttccagggt ttcacagcaa cccgcgtgta      660
gacctgaate tgccccctat cgtaattat aaatatagtg gtagtaattc actcgacatg      720
tgtttctatg atggatatag taaaaacagt gatagcatgg taataaagtt ccaggatgat      780
aatcctacca attcatctga atataatctt tataagatag ggggcaactga aaaattacca      840
tatgtgtttt cactgcttat gggagaaaaa atattttatc cagtgaatgg tcaatcattt      900
actatcaatg acagtagtgt actcgaaca aactggaatc gagtaaccgc agttgctatg      960
ccggaagtta atgttccagt attatgctgg ccagcaagat tgctattaaa tgctgatgta     1020
aatgtcccg atgcaggaca gtattcagga cagatatata taacatttac acccagtgtc     1080
gaaaatttat ga                                                                1092

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<210> SEQ ID NO 75
<211> LENGTH: 363
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 75
Met Lys Lys Ile Phe Ile Phe Leu Ser Ile Ile Phe Ser Ala Val Val
 1             5             10            15
Ser Ala Gly Arg Tyr Pro Glu Thr Thr Val Gly Asn Leu Thr Lys Ser
 20            25            30
Phe Gln Ala Pro Arg Leu Asp Arg Ser Val Gln Ser Pro Ile Tyr Asn
 35            40            45
Ile Phe Thr Asn His Val Ala Gly Tyr Ser Leu Ser His Ser Leu Tyr
 50            55            60
Asp Arg Ile Val Phe Leu Cys Thr Ser Ser Ser Asn Pro Val Asn Gly
 65            70            75            80
Ala Cys Pro Thr Ile Gly Thr Ser Gly Val Gln Tyr Gly Thr Thr Thr
 85            90            95
Ile Thr Leu Gln Phe Thr Glu Lys Arg Ser Leu Ile Lys Arg Asn Ile
 100           105           110
Asn Leu Ala Gly Asn Lys Lys Pro Ile Trp Glu Asn Gln Ser Cys Asp
 115           120           125

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Phe Ser Asn Leu Met Val Leu Asn Ser Lys Ser Trp Ser Cys Gly Ala  
 130 135 140

Tyr Gly Asn Ala Asn Gly Thr Leu Leu Asn Leu Tyr Ile Pro Ala Gly  
 145 150 155 160

Glu Ile Asn Lys Leu Pro Phe Gly Gly Ile Trp Glu Ala Thr Leu Ile  
 165 170 175

Leu Arg Leu Ser Arg Tyr Gly Glu Val Ser Ser Thr His Tyr Gly Asn  
 180 185 190

Tyr Thr Val Asn Ile Thr Val Asp Leu Thr Asp Lys Gly Asn Ile Gln  
 195 200 205

Val Trp Leu Pro Gly Phe His Ser Asn Pro Arg Val Asp Leu Asn Leu  
 210 215 220

Arg Pro Ile Gly Asn Tyr Lys Tyr Ser Gly Ser Asn Ser Leu Asp Met  
 225 230 235 240

Cys Phe Tyr Asp Gly Tyr Ser Thr Asn Ser Asp Ser Met Val Ile Lys  
 245 250 255

Phe Gln Asp Asp Asn Pro Thr Asn Ser Ser Glu Tyr Asn Leu Tyr Lys  
 260 265 270

Ile Gly Gly Thr Glu Lys Leu Pro Tyr Ala Val Ser Leu Leu Met Gly  
 275 280 285

Glu Lys Ile Phe Tyr Pro Val Asn Gly Gln Ser Phe Thr Ile Asn Asp  
 290 295 300

Ser Ser Val Leu Glu Thr Asn Trp Asn Arg Val Thr Ala Val Ala Met  
 305 310 315 320

Pro Glu Val Asn Val Pro Val Leu Cys Trp Pro Ala Arg Leu Leu Leu  
 325 330 335

Asn Ala Asp Val Asn Ala Pro Asp Ala Gly Gln Tyr Ser Gly Gln Ile  
 340 345 350

Tyr Ile Thr Phe Thr Pro Ser Val Glu Asn Leu  
 355 360

<210> SEQ ID NO 76  
 <211> LENGTH: 501  
 <212> TYPE: DNA  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 76

```

atgaaaactga agaaaaacaat tggcgcgaatg gctatggcga ctctgtttgc caccatggct    60
gcctctgcag tcgaaaaaaaa tattactgtg agggcaagtg ttgaccctaa acttgatcct    120
ctgcaagcag atggaacttc actgccggac tctatcgcat taacctattc ttcggcttca    180
aataattttg aagtttactc tcttaatact gctattcata caaatgacaa aaccaaggca    240
gttgtagtga agctgtcagc tccagcagtt ctgtccaata ttatgaagcc aagctcgcaa    300
attccgatga aagtgacttt gggggggaag acgctgagta cagctgatgc tgagtttgct    360
gctgatactc tgaactttgg tgcacatcggg gttgaaaacg tttcttcctg tcaacagcct    420
acgattcatg cagaagctgc tccgctgag gcaggaatt accaaggtgt tatttctctt    480
atcatgactc aaaaaactta a                                     501
    
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<210> SEQ ID NO 77  
 <211> LENGTH: 166  
 <212> TYPE: PRT  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 77

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Met Lys Leu Lys Lys Thr Ile Gly Ala Met Ala Met Ala Thr Leu Phe  
 1 5 10 15  
 Ala Thr Met Ala Ala Ser Ala Val Glu Lys Asn Ile Thr Val Arg Ala  
 20 25 30  
 Ser Val Asp Pro Lys Leu Asp Leu Leu Gln Ala Asp Gly Thr Ser Leu  
 35 40 45  
 Pro Asp Ser Ile Ala Leu Thr Tyr Ser Ser Ala Ser Asn Asn Phe Glu  
 50 55 60  
 Val Tyr Ser Leu Asn Thr Ala Ile His Thr Asn Asp Lys Thr Lys Ala  
 65 70 75 80  
 Val Val Val Lys Leu Ser Ala Pro Ala Val Leu Ser Asn Ile Met Lys  
 85 90 95  
 Pro Ser Ser Gln Ile Pro Met Lys Val Thr Leu Gly Gly Lys Thr Leu  
 100 105 110  
 Ser Thr Ala Asp Ala Glu Phe Ala Ala Asp Thr Leu Asn Phe Gly Ala  
 115 120 125  
 Ser Gly Val Glu Asn Val Ser Ser Val Gln Gln Leu Thr Ile His Ala  
 130 135 140  
 Glu Ala Ala Pro Pro Glu Ala Gly Asn Tyr Gln Gly Val Ile Ser Leu  
 145 150 155 160  
 Ile Met Thr Gln Lys Thr  
 165

<210> SEQ ID NO 78  
 <211> LENGTH: 1092  
 <212> TYPE: DNA  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 78

atgaaaaaga tatttatttt tttgtctatc atattttctg cggtggtcag tgccgggcca 60  
 taccocgaaa ctacagtagg taatctgacg aagagttttc aagcccctcg tctggataga 120  
 agcgtacaat caccaatata taacatcttt acgaatcatg tggctggata tagtttgagt 180  
 catagattat atgacaggat tgtttttgta tgtacatcct cgtcgaatcc ggttaatggt 240  
 gcttgcccaa ccattggaac atctagagtt gaatacggta ctacaacccat aaccttgacg 300  
 tttacagaaa aaagaagtct gataaaaaga aatattaatc ttgcaggtaa taagaaacca 360  
 atatgggaga atcagagttg cgacactagc aatctaattg tgmtgaattc gaagtcttgg 420  
 tcctgtgggg ctctaggaaa tgctaacgga acacttctaa atctgtatat ccctgcagga 480  
 gaaatcaaca aattgccttt tggagggata tgggaggcaa ctctgatctt acgcttatca 540  
 agatatggcg aagtcagtag caccattac ggcaattata ccgtaaatat tacggttgat 600  
 ttaactgata aagtaatat tcaggtatgg cttccagggt ttcacagcaa cccgcgtgta 660  
 gacctgaatc tgcaccctat cgtaattat aaatatagtg gtagtaattc actcgacatg 720  
 tgtttctatg atggatatag tacaacacgt gatagcatgg taataaagtt ccaggatgat 780  
 aatcctacca attcatctga atataatctt tataagatag ggggcaactga aaaattacca 840  
 tatgtgtgtt cactgcttat gggaggaaaa atattttatc cagtgaatgg tcaatcattt 900  
 actatcaatg acagtagtgt actcgaaca aactggaatc gagtaaccgc agttgctatg 960  
 ccggaagtta atgttccagt attatgctgg ccagcaagat tgctattaaa tgctgatgta 1020  
 aatgtcccgc atgcaggaca gtattcagga cagatatata taacatttac acccagtgtc 1080  
 gaaaatttat ga 1092

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<210> SEQ ID NO 79  
 <211> LENGTH: 363  
 <212> TYPE: PRT  
 <213> ORGANISM: Escherichia coli  
  
 <400> SEQUENCE: 79  
  
 Met Lys Lys Ile Phe Ile Phe Leu Ser Ile Ile Phe Ser Ala Val Val  
 1 5 10 15  
  
 Ser Ala Gly Arg Tyr Pro Glu Thr Thr Val Gly Asn Leu Thr Lys Ser  
 20 25 30  
  
 Phe Gln Ala Pro Arg Leu Asp Arg Ser Val Gln Ser Pro Ile Tyr Asn  
 35 40 45  
  
 Ile Phe Thr Asn His Val Ala Gly Tyr Ser Leu Ser His Arg Leu Tyr  
 50 55 60  
  
 Asp Arg Ile Val Phe Val Cys Thr Ser Ser Ser Asn Pro Val Asn Gly  
 65 70 75 80  
  
 Ala Cys Pro Thr Ile Gly Thr Ser Arg Val Glu Tyr Gly Thr Thr Thr  
 85 90 95  
  
 Ile Thr Leu Gln Phe Thr Glu Lys Arg Ser Leu Ile Lys Arg Asn Ile  
 100 105 110  
  
 Asn Leu Ala Gly Asn Lys Lys Pro Ile Trp Glu Asn Gln Ser Cys Asp  
 115 120 125  
  
 Thr Ser Asn Leu Met Val Leu Asn Ser Lys Ser Trp Ser Cys Gly Ala  
 130 135 140  
  
 Leu Gly Asn Ala Asn Gly Thr Leu Leu Asn Leu Tyr Ile Pro Ala Gly  
 145 150 155 160  
  
 Glu Ile Asn Lys Leu Pro Phe Gly Gly Ile Trp Glu Ala Thr Leu Ile  
 165 170 175  
  
 Leu Arg Leu Ser Arg Tyr Gly Glu Val Ser Ser Thr His Tyr Gly Asn  
 180 185 190  
  
 Tyr Thr Val Asn Ile Thr Val Asp Leu Thr Asp Lys Gly Asn Ile Gln  
 195 200 205  
  
 Val Trp Leu Pro Gly Phe His Ser Asn Pro Arg Val Asp Leu Asn Leu  
 210 215 220  
  
 His Pro Ile Gly Asn Tyr Lys Tyr Ser Gly Ser Asn Ser Leu Asp Met  
 225 230 235 240  
  
 Cys Phe Tyr Asp Gly Tyr Ser Thr Asn Ser Asp Ser Met Val Ile Lys  
 245 250 255  
  
 Phe Gln Asp Asp Asn Pro Thr Asn Ser Ser Glu Tyr Asn Leu Tyr Lys  
 260 265 270  
  
 Ile Gly Gly Thr Glu Lys Leu Pro Tyr Ala Val Ser Leu Leu Met Gly  
 275 280 285  
  
 Gly Lys Ile Phe Tyr Pro Val Asn Gly Gln Ser Phe Thr Ile Asn Asp  
 290 295 300  
  
 Ser Ser Val Leu Glu Thr Asn Trp Asn Arg Val Thr Ala Val Ala Met  
 305 310 315 320  
  
 Pro Glu Val Asn Val Pro Val Leu Cys Trp Pro Ala Arg Leu Leu Leu  
 325 330 335  
  
 Asn Ala Asp Val Asn Ala Pro Asp Ala Gly Gln Tyr Ser Gly Gln Ile  
 340 345 350  
  
 Tyr Ile Thr Phe Thr Pro Ser Val Glu Asn Leu  
 355 360

&lt;210&gt; SEQ ID NO 80

-continued

<211> LENGTH: 513  
 <212> TYPE: DNA  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 80

```

atgaaactaa agaaaacaat tggcgcaatg gctctggcga cattatttgc aaccatggga      60
gcatctgctg tcgagaagac cattagcgtt acggcgagtg ttgacccgac tgttgacctt      120
ctgcaatctg atggctctgc gctgccgaac tctgtcgcac taacctattc tccggtgtga      180
gggggttttg aagctcacac catcaacacc gttgttcata caaatgaccc agctaaaggt      240
gttattgtga agctgtcagc agaaccagtc ctgtccaatg tactgaatcc aacctgcaa      300
attctgtttt ctgtgaattt cgcaggaaaa aaactgacca caacaggcac taccatcgaa      360
tccaataaac tgaactttgc ttcgagtggg gttgataaag tttcttctac gcagaaactt      420
tcaatccatg cagatactac tcaggttaact ggcggactaa cagctgggtca atatcagggg      480
ctcgtatcaa ttatcctgac tcagtcaacg taa                                     513
    
```

<210> SEQ ID NO 81  
 <211> LENGTH: 170  
 <212> TYPE: PRT  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 81

```

Met Lys Leu Lys Lys Thr Ile Gly Ala Met Ala Leu Ala Thr Leu Phe
 1           5           10          15
Ala Thr Met Gly Ala Ser Ala Val Glu Lys Thr Ile Ser Val Thr Ala
 20          25          30
Ser Val Asp Pro Thr Val Asp Leu Leu Gln Ser Asp Gly Ser Ala Leu
 35          40          45
Pro Asn Ser Val Ala Leu Thr Tyr Ser Pro Ala Val Gly Gly Phe Glu
 50          55          60
Ala His Thr Ile Asn Thr Val Val His Thr Asn Asp Pro Ala Lys Gly
 65          70          75          80
Val Ile Val Lys Leu Ser Ala Glu Pro Val Leu Ser Asn Val Leu Asn
 85          90          95
Pro Thr Leu Gln Ile Pro Val Ser Val Asn Phe Ala Gly Lys Lys Leu
100         105         110
Thr Thr Thr Gly Thr Thr Ile Glu Ser Asn Lys Leu Asn Phe Ala Ser
115         120         125
Ser Gly Val Asp Lys Val Ser Ser Thr Gln Lys Leu Ser Ile His Ala
130         135         140
Asp Thr Thr Gln Val Thr Gly Gly Leu Thr Ala Gly Gln Tyr Gln Gly
145         150         155         160
Leu Val Ser Ile Ile Leu Thr Gln Ser Thr
165         170
    
```

<210> SEQ ID NO 82  
 <211> LENGTH: 1092  
 <212> TYPE: DNA  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 82

```

atgaaaaaga tatttatttt tttgtctatc atattttctg cgggtggtcag tgccgggcca      60
taccocggaaa ctacagtagg taatctgacg aagagttttc aagcccctcg tctggataga      120
agcgtacaat caccaatata taacatcttt acgaatcatg tggctggata tagtttgagt      180
    
```

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catagattat atgacaggat tgtttttgta tgtacatcct cgtcgaatcc ggtaaatggt 240
gcttgcccaa ccattggaac atctggagtt gaatacggta ctacaacat aaccttgag 300
tttacagaaa aaagaagtct gataaaaaga aatattaatc ttgcaggtaa taagaaacca 360
atatgggaga atcagagttg cgactttagc aatctaattg tgttgaattc gaagtcttg 420
tcctgtgggg ctcaaggaaa tgtaacgga acacttctaa atctgtatat ccctgcagga 480
gaaatcaaca aattgccttt tggagggata tgggaggcaa ctctgatctt acgcttatca 540
agatatggcg aagtcagtag caccattac ggcaattata ccgtaaatat tacggttgat 600
ttaactgata aaggtaatat tcaggtatgg cttccagggt ttcacagcaa cccgcgtgta 660
gacctgaatc tgcacctat cgtaattat aaatatagtg gtagtaattc actcgacatg 720
tgtttctatg atggatatag tacaacagt gatagcatgg taataaagtt ccaggatgat 780
aatcctacca attcatctga atataatctt tataagagag ggggcaactga aaaattacca 840
tatgtgtttt cactgcttat gggaggaaaa atattttatc cagtgaatgg tcaatcattt 900
actatcaatg acagtagtgt actcgaaca aactggaatc gagtaaccgc agttgctatg 960
ccggaagtta atgttccagt attatgctgg ccagcaagat tgctattaaa tgctgatgta 1020
aatgtcccg atgcaggaca gtattcagga cagatatata taacatttac acccagtgtc 1080
gaaaatttat ga 1092
    
```

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<210> SEQ ID NO 83
<211> LENGTH: 363
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli
    
```

<400> SEQUENCE: 83

```

Met Lys Lys Ile Phe Ile Phe Leu Ser Ile Ile Phe Ser Ala Val Val
 1             5             10            15
Ser Ala Gly Arg Tyr Pro Glu Thr Thr Val Gly Asn Leu Thr Lys Ser
      20            25            30
Phe Gln Ala Pro Arg Leu Asp Arg Ser Val Gln Ser Pro Ile Tyr Asn
      35            40            45
Ile Phe Thr Asn His Val Ala Gly Tyr Ser Leu Ser His Arg Leu Tyr
      50            55            60
Asp Arg Ile Val Phe Val Cys Thr Ser Ser Ser Asn Pro Val Asn Gly
 65            70            75            80
Ala Cys Pro Thr Ile Gly Thr Ser Gly Val Glu Tyr Gly Thr Thr Thr
      85            90            95
Ile Thr Leu Gln Phe Thr Glu Lys Arg Ser Leu Ile Lys Arg Asn Ile
      100           105           110
Asn Leu Ala Gly Asn Lys Lys Pro Ile Trp Glu Asn Gln Ser Cys Asp
      115           120           125
Phe Ser Asn Leu Met Val Leu Asn Ser Lys Ser Trp Ser Cys Gly Ala
      130           135           140
Gln Gly Asn Ala Asn Gly Thr Leu Leu Asn Leu Tyr Ile Pro Ala Gly
 145           150           155           160
Glu Ile Asn Lys Leu Pro Phe Gly Gly Ile Trp Glu Ala Thr Leu Ile
      165           170           175
Leu Arg Leu Ser Arg Tyr Gly Glu Val Ser Ser Thr His Tyr Gly Asn
      180           185           190
Tyr Thr Val Asn Ile Thr Val Asp Leu Thr Asp Lys Gly Asn Ile Gln
      195           200           205
    
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Val Trp Leu Pro Gly Phe His Ser Asn Pro Arg Val Asp Leu Asn Leu  
 210 215 220

His Pro Ile Gly Asn Tyr Lys Tyr Ser Gly Ser Asn Ser Leu Asp Met  
 225 230 235 240

Cys Phe Tyr Asp Gly Tyr Ser Thr Asn Ser Asp Ser Met Val Ile Lys  
 245 250 255

Phe Gln Asp Asp Asn Pro Thr Asn Ser Ser Glu Tyr Asn Leu Tyr Lys  
 260 265 270

Arg Gly Gly Thr Glu Lys Leu Pro Tyr Ala Val Ser Leu Leu Met Gly  
 275 280 285

Gly Lys Ile Phe Tyr Pro Val Asn Gly Gln Ser Phe Thr Ile Asn Asp  
 290 295 300

Ser Ser Val Leu Glu Thr Asn Trp Asn Arg Val Thr Ala Val Ala Met  
 305 310 315 320

Pro Glu Val Asn Val Pro Val Leu Cys Trp Pro Ala Arg Leu Leu Leu  
 325 330 335

Asn Ala Asp Val Asn Ala Pro Asp Ala Gly Gln Tyr Ser Gly Gln Ile  
 340 345 350

Tyr Ile Thr Phe Thr Pro Ser Val Glu Asn Leu  
 355 360

<210> SEQ ID NO 84  
 <211> LENGTH: 507  
 <212> TYPE: DNA  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 84

```

atggttaaaaa taaaataactt attaataaggt ctttcactgt cagctatgag ttcataactca    60
ctagetgcag cgggggccac tctaaccaaa gaactggcat taaatgtgct ttctcctgca    120
gctctggatg caacttgggc tcctcaggat aatttaacat tatccaatac tggcgtttct    180
aatactttgg tgggtgtttt gactctttca aataccagta ttgatacagt tagcattgcg    240
agtacaaaatg tttctgatac atctaagaat ggtacagtaa cttttgcaca tgagacaaat    300
aactctgcta gctttgccac caccatttca acagataatg ccaacattac gttggataaa    360
aatgctggaa atacgattgt taaaactaca aatgggagtc agttgccaac taatttacca    420
cttaagttta ttaccactga aggtaacgaa catttagttt caggtaatta ccgtgcaaat    480
ataacaatta cttcgacaat taataaa                                     507
    
```

<210> SEQ ID NO 85  
 <211> LENGTH: 168  
 <212> TYPE: PRT  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 85

Met Leu Lys Ile Lys Tyr Leu Leu Ile Gly Leu Ser Leu Ser Ala Met  
 1 5 10 15

Ser Ser Tyr Ser Leu Ala Ala Ala Gly Pro Thr Leu Thr Lys Glu Leu  
 20 25 30

Ala Leu Asn Val Leu Ser Pro Ala Ala Leu Asp Ala Thr Trp Ala Pro  
 35 40 45

Gln Asp Asn Leu Thr Leu Ser Asn Thr Gly Val Ser Asn Thr Leu Val  
 50 55 60

Gly Val Leu Thr Leu Ser Asn Thr Ser Ile Asp Thr Val Ser Ile Ala  
 65 70 75 80



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<210> SEQ ID NO 88  
 <211> LENGTH: 339  
 <212> TYPE: PRT  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 88

Ala Asp Lys Ile Pro Gly Asp Glu Ser Ile Thr Asn Ile Phe Gly Pro  
 1 5 10 15  
 Arg Asp Arg Asn Glu Ser Ser Pro Lys His Asn Ile Leu Asn Asn His  
 20 25 30  
 Ile Thr Ala Tyr Ser Glu Ser His Thr Leu Tyr Asp Arg Met Thr Phe  
 35 40 45  
 Leu Cys Leu Ser Ser His Asn Thr Leu Asn Gly Ala Cys Pro Thr Ser  
 50 55 60  
 Glu Asn Pro Ser Ser Ser Ser Val Ser Gly Glu Thr Asn Ile Thr Leu  
 65 70 75 80  
 Gln Phe Thr Glu Lys Arg Ser Leu Ile Lys Arg Glu Leu Gln Ile Lys  
 85 90 95  
 Gly Tyr Lys Gln Leu Leu Phe Lys Ser Val Asn Cys Pro Ser Gly Leu  
 100 105 110  
 Thr Leu Asn Ser Ala His Phe Asn Cys Asn Lys Asn Ala Ala Ser Gly  
 115 120 125  
 Ala Ser Leu Tyr Leu Tyr Ile Pro Ala Gly Glu Leu Lys Asn Leu Pro  
 130 135 140  
 Phe Gly Gly Ile Trp Asp Ala Thr Leu Lys Leu Arg Val Lys Arg Arg  
 145 150 155 160  
 Tyr Ser Glu Thr Tyr Gly Thr Tyr Thr Ile Asn Ile Thr Ile Lys Leu  
 165 170 175  
 Thr Asp Lys Gly Asn Ile Gln Ile Trp Leu Pro Gln Phe Lys Ser Asp  
 180 185 190  
 Ala Arg Val Asp Leu Asn Leu Arg Pro Thr Gly Gly Gly Thr Tyr Ile  
 195 200 205  
 Gly Arg Asn Ser Val Asp Met Cys Phe Tyr Asp Gly Tyr Ser Thr Asn  
 210 215 220  
 Ser Ser Ser Leu Glu Ile Arg Phe Gln Asp Asn Asn Pro Lys Ser Asp  
 225 230 235 240  
 Gly Lys Phe Tyr Leu Arg Lys Ile Asn Asp Asp Thr Lys Glu Ile Ala  
 245 250 255  
 Tyr Thr Leu Ser Leu Leu Leu Ala Gly Lys Ser Leu Thr Pro Thr Asn  
 260 265 270  
 Gly Thr Ser Leu Asn Ile Ala Asp Ala Ala Ser Leu Glu Thr Asn Trp  
 275 280 285  
 Asn Arg Ile Thr Ala Val Thr Met Pro Glu Ile Ser Val Pro Val Leu  
 290 295 300  
 Cys Trp Pro Gly Arg Leu Gln Leu Asp Ala Lys Val Glu Asn Pro Glu  
 305 310 315 320  
 Ala Gly Gln Tyr Met Gly Asn Ile Asn Val Thr Phe Thr Pro Ser Ser  
 325 330 335  
 Gln Thr Leu

<210> SEQ ID NO 89  
 <211> LENGTH: 144  
 <212> TYPE: PRT  
 <213> ORGANISM: Escherichia coli

-continued

&lt;400&gt; SEQUENCE: 89

Val Glu Lys Asn Ile Thr Val Thr Ala Ser Val Asp Pro Thr Ile Asp  
 1 5 10 15  
 Ile Leu Gln Ala Asp Gly Ser Ser Leu Pro Thr Ala Val Glu Leu Thr  
 20 25 30  
 Tyr Ser Pro Ala Ala Ser Arg Phe Glu Asn Tyr Lys Ile Ala Thr Lys  
 35 40 45  
 Val His Thr Asn Val Ile Asn Lys Asn Val Leu Val Lys Leu Val Asn  
 50 55 60  
 Asp Pro Lys Leu Thr Asn Val Leu Asp Ser Thr Lys Gln Leu Pro Ile  
 65 70 75 80  
 Thr Val Ser Tyr Gly Gly Lys Thr Leu Ser Thr Ala Asp Val Thr Phe  
 85 90 95  
 Glu Pro Ala Glu Leu Asn Phe Gly Thr Ser Gly Val Thr Gly Val Ser  
 100 105 110  
 Ser Ser Gln Asp Leu Val Ile Gly Ala Thr Thr Ala Gln Ala Pro Thr  
 115 120 125  
 Ala Gly Asn Tyr Ser Gly Val Val Ser Ile Leu Met Thr Leu Ala Ser  
 130 135 140

&lt;210&gt; SEQ ID NO 90

&lt;211&gt; LENGTH: 339

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Escherichia coli

&lt;400&gt; SEQUENCE: 90

Ala Asp Lys Ile Pro Gly Asp Glu Asn Ile Thr Asn Ile Phe Gly Pro  
 1 5 10 15  
 Arg Asp Arg Asn Glu Ser Ser Pro Lys His Asn Ile Leu Asn Asp Tyr  
 20 25 30  
 Ile Thr Ala Tyr Ser Glu Ser His Thr Leu Tyr Asp Arg Met Ile Phe  
 35 40 45  
 Leu Cys Leu Ser Ser Gln Asn Thr Leu Asn Gly Ala Cys Pro Thr Ser  
 50 55 60  
 Glu Asn Pro Ser Ser Ser Val Ser Gly Glu Thr Asn Ile Thr Leu  
 65 70 75 80  
 Gln Phe Thr Glu Lys Arg Ser Leu Ile Lys Arg Glu Leu Gln Ile Lys  
 85 90 95  
 Gly Tyr Lys Arg Leu Leu Phe Lys Gly Ala Asn Cys Pro Ser Tyr Leu  
 100 105 110  
 Thr Leu Asn Ser Ala His Tyr Thr Cys Asn Arg Asn Ser Ala Ser Gly  
 115 120 125  
 Ala Ser Leu Tyr Leu Tyr Ile Pro Ala Gly Glu Leu Lys Asn Leu Pro  
 130 135 140  
 Phe Gly Gly Ile Trp Asp Ala Thr Leu Lys Leu Arg Val Lys Arg Arg  
 145 150 155 160  
 Tyr Asp Gln Thr Tyr Gly Thr Tyr Thr Ile Asn Ile Thr Val Lys Leu  
 165 170 175  
 Thr Asp Lys Gly Asn Ile Gln Ile Trp Leu Pro Gln Phe Lys Ser Asp  
 180 185 190  
 Ala Arg Val Asp Leu Asn Leu Arg Pro Thr Gly Gly Gly Thr Tyr Ile  
 195 200 205  
 Gly Arg Asn Ser Val Asp Met Cys Phe Tyr Asp Gly Tyr Ser Thr Asn  
 210 215 220

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Ser Ser Ser Leu Glu Leu Arg Phe Gln Asp Asn Asn Pro Lys Ser Asp  
 225 230 235 240

Gly Lys Phe Tyr Leu Arg Lys Ile Asn Asp Asp Thr Lys Glu Ile Ala  
 245 250 255

Tyr Thr Leu Ser Leu Leu Leu Ala Gly Lys Ser Leu Thr Pro Thr Asn  
 260 265 270

Gly Thr Ser Leu Asn Ile Ala Asp Ala Ala Ser Leu Glu Ile Asn Trp  
 275 280 285

Asn Arg Ile Thr Ala Val Thr Met Pro Glu Ile Ser Val Pro Val Leu  
 290 295 300

Cys Trp Pro Gly Arg Leu Gln Leu Asp Ala Lys Val Glu Asn Pro Glu  
 305 310 315 320

Ala Gly Gln Tyr Met Gly Asn Ile Asn Ile Thr Phe Thr Pro Ser Ser  
 325 330 335

Gln Thr Leu

<210> SEQ ID NO 91  
 <211> LENGTH: 152  
 <212> TYPE: PRT  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 91

Val Glu Lys Asn Ile Thr Val Thr Ala Ser Val Asp Pro Thr Ile Asp  
 1 5 10 15

Ile Leu Gln Ala Asn Gly Ser Ala Leu Pro Thr Ala Val Asp Leu Thr  
 20 25 30

Tyr Leu Pro Gly Ala Lys Thr Phe Glu Asn Tyr Ser Val Leu Thr Gln  
 35 40 45

Ile Tyr Thr Asn Asp Pro Ser Lys Gly Leu Asp Val Arg Leu Val Asp  
 50 55 60

Thr Pro Lys Leu Thr Asn Ile Leu Gln Pro Thr Ser Thr Ile Pro Leu  
 65 70 75 80

Thr Val Ser Trp Ala Gly Lys Thr Leu Ser Thr Ser Ala Gln Lys Ile  
 85 90 95

Ala Val Gly Asp Leu Gly Phe Gly Ser Thr Gly Thr Ala Gly Val Ser  
 100 105 110

Asn Ser Lys Glu Leu Val Ile Gly Ala Thr Thr Ser Gly Thr Ala Pro  
 115 120 125

Ser Ala Gly Lys Tyr Gln Gly Val Val Ser Ile Val Met Thr Gln Ser  
 130 135 140

Thr Asp Thr Ala Ala Pro Val Pro  
 145 150

<210> SEQ ID NO 92  
 <211> LENGTH: 146  
 <212> TYPE: PRT  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 92

Val Glu Lys Asn Ile Thr Val Thr Ala Ser Val Asp Pro Thr Ile Asp  
 1 5 10 15

Ile Leu Gln Ala Asn Gly Ser Ala Leu Pro Thr Ala Val Asp Leu Thr  
 20 25 30

Tyr Leu Pro Gly Ala Lys Thr Phe Glu Asn Tyr Ser Val Leu Thr Gln  
 35 40 45

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Ile Tyr Thr Asn Asp Pro Ser Lys Gly Leu Asp Val Arg Leu Val Asp
 50                               55                               60

Thr Pro Lys Leu Thr Asn Ile Leu Gln Pro Thr Ser Thr Ile Pro Leu
65                               70                               75                               80

Thr Val Ser Trp Ala Gly Arg Thr Leu Ser Thr Ser Ala Gln Lys Ile
                               85                               90                               95

Ala Val Gly Asp Leu Gly Phe Gly Ser Thr Gly Thr Ala Gly Val Ser
                               100                               105                               110

Asn Ser Lys Glu Leu Val Ile Gly Ala Thr Thr Ser Gly Thr Ala Pro
                               115                               120                               125

Ser Ala Gly Lys Tyr Gln Gly Val Val Ser Ile Val Met Thr Gln Ser
                               130                               135                               140

Thr Asn
145

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<210> SEQ ID NO 93
<211> LENGTH: 345
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

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<400> SEQUENCE: 93

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Gly Arg Tyr Pro Glu Thr Thr Val Gly Asn Leu Thr Lys Ser Phe Gln
 1                               5                               10                               15

Ala Pro Arg Leu Asp Arg Ser Val Gln Ser Pro Ile Tyr Asn Ile Phe
                               20                               25                               30

Thr Asn His Val Ala Gly Tyr Ser Leu Ser His Ser Leu Tyr Asp Arg
                               35                               40                               45

Ile Val Phe Leu Cys Thr Ser Ser Ser Asn Pro Val Asn Gly Ala Cys
 50                               55                               60

Pro Thr Ile Gly Thr Ser Gly Val Gln Tyr Gly Thr Thr Thr Ile Thr
65                               70                               75                               80

Leu Gln Phe Thr Glu Lys Arg Ser Leu Ile Lys Arg Asn Ile Asn Leu
                               85                               90                               95

Ala Gly Asn Lys Lys Pro Ile Trp Glu Asn Gln Ser Cys Asp Phe Ser
                               100                               105                               110

Asn Leu Met Val Leu Asn Ser Lys Ser Trp Ser Cys Gly Ala Tyr Gly
                               115                               120                               125

Asn Ala Asn Gly Thr Leu Leu Asn Leu Tyr Ile Pro Ala Gly Glu Ile
                               130                               135                               140

Asn Lys Leu Pro Phe Gly Gly Ile Trp Glu Ala Thr Leu Ile Leu Arg
145                               150                               155                               160

Leu Ser Arg Tyr Gly Glu Val Ser Ser Thr His Tyr Gly Asn Tyr Thr
                               165                               170                               175

Val Asn Ile Thr Val Asp Leu Thr Asp Lys Gly Asn Ile Gln Val Trp
                               180                               185                               190

Leu Pro Gly Phe His Ser Asn Pro Arg Val Asp Leu Asn Leu Arg Pro
                               195                               200                               205

Ile Gly Asn Tyr Lys Tyr Ser Gly Ser Asn Ser Leu Asp Met Cys Phe
                               210                               215                               220

Tyr Asp Gly Tyr Ser Thr Asn Ser Asp Ser Met Val Ile Lys Phe Gln
225                               230                               235                               240

Asp Asp Asn Pro Thr Asn Ser Ser Glu Tyr Asn Leu Tyr Lys Ile Gly
                               245                               250                               255

Gly Thr Glu Lys Leu Pro Tyr Ala Val Ser Leu Leu Met Gly Glu Lys
                               260                               265                               270

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Ile Phe Tyr Pro Val Asn Gly Gln Ser Phe Thr Ile Asn Asp Ser Ser  
 275 280 285  
 Val Leu Glu Thr Asn Trp Asn Arg Val Thr Ala Val Ala Met Pro Glu  
 290 295 300  
 Val Asn Val Pro Val Leu Cys Trp Pro Ala Arg Leu Leu Leu Asn Ala  
 305 310 315 320  
 Asp Val Asn Ala Pro Asp Ala Gly Gln Tyr Ser Gly Gln Ile Tyr Ile  
 325 330 335  
 Thr Phe Thr Pro Ser Val Glu Asn Leu  
 340 345

<210> SEQ ID NO 94  
 <211> LENGTH: 148  
 <212> TYPE: PRT  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 94

Val Glu Lys Thr Ile Ser Val Thr Ala Ser Val Asp Pro Thr Val Asp  
 1 5 10 15  
 Leu Leu Gln Ser Asp Gly Ser Ala Leu Pro Asn Ser Val Ala Leu Thr  
 20 25 30  
 Tyr Ser Pro Ala Val Asn Asn Phe Glu Ala His Thr Ile Asn Thr Val  
 35 40 45  
 Val His Thr Asn Asp Ser Asp Lys Gly Val Val Val Lys Leu Ser Ala  
 50 55 60  
 Asp Pro Val Leu Ser Asn Val Leu Asn Pro Thr Leu Gln Ile Pro Val  
 65 70 75 80  
 Ser Val Asn Phe Ala Gly Lys Pro Leu Ser Thr Thr Gly Ile Thr Ile  
 85 90 95  
 Asp Ser Asn Asp Leu Asn Phe Ala Ser Ser Gly Val Asn Lys Val Ser  
 100 105 110  
 Ser Thr Gln Lys Leu Ser Ile His Ala Asp Ala Thr Arg Val Thr Gly  
 115 120 125  
 Gly Ala Leu Thr Ala Gly Gln Tyr Gln Gly Leu Val Ser Ile Ile Leu  
 130 135 140  
 Thr Lys Ser Thr  
 145

<210> SEQ ID NO 95  
 <211> LENGTH: 345  
 <212> TYPE: PRT  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 95

Gly Arg Tyr Pro Glu Thr Thr Val Gly Asn Leu Thr Lys Ser Phe Gln  
 1 5 10 15  
 Ala Pro Arg Leu Asp Arg Ser Val Gln Ser Pro Ile Tyr Asn Ile Phe  
 20 25 30  
 Thr Asn His Val Ala Gly Tyr Ser Leu Ser His Arg Leu Tyr Asp Arg  
 35 40 45  
 Ile Val Phe Val Cys Thr Ser Ser Ser Asn Pro Val Asn Gly Ala Cys  
 50 55 60  
 Pro Thr Ile Gly Thr Ser Arg Val Glu Tyr Gly Thr Thr Thr Ile Thr  
 65 70 75 80  
 Leu Gln Phe Thr Glu Lys Arg Ser Leu Ile Lys Arg Asn Ile Asn Leu  
 85 90 95

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Ala Gly Asn Lys Lys Pro Ile Trp Glu Asn Gln Ser Cys Asp Thr Ser  
 100 105 110

Asn Leu Met Val Leu Asn Ser Lys Ser Trp Ser Cys Gly Ala Leu Gly  
 115 120 125

Asn Ala Asn Gly Thr Leu Leu Asn Leu Tyr Ile Pro Ala Gly Glu Ile  
 130 135 140

Asn Lys Leu Pro Phe Gly Gly Ile Trp Glu Ala Thr Leu Ile Leu Arg  
 145 150 155 160

Leu Ser Arg Tyr Gly Glu Val Ser Ser Thr His Tyr Gly Asn Tyr Thr  
 165 170 175

Val Asn Ile Thr Val Asp Leu Thr Asp Lys Gly Asn Ile Gln Val Trp  
 180 185 190

Leu Pro Gly Phe His Ser Asn Pro Arg Val Asp Leu Asn Leu His Pro  
 195 200 205

Ile Gly Asn Tyr Lys Tyr Ser Gly Ser Asn Ser Leu Asp Met Cys Phe  
 210 215 220

Tyr Asp Gly Tyr Ser Thr Asn Ser Asp Ser Met Val Ile Lys Phe Gln  
 225 230 235 240

Asp Asp Asn Pro Thr Asn Ser Ser Glu Tyr Asn Leu Tyr Lys Ile Gly  
 245 250 255

Gly Thr Glu Lys Leu Pro Tyr Ala Val Ser Leu Leu Met Gly Gly Lys  
 260 265 270

Ile Phe Tyr Pro Val Asn Gly Gln Ser Phe Thr Ile Asn Asp Ser Ser  
 275 280 285

Val Leu Glu Thr Asn Trp Asn Arg Val Thr Ala Val Ala Met Pro Glu  
 290 295 300

Val Asn Val Pro Val Leu Cys Trp Pro Ala Arg Leu Leu Leu Asn Ala  
 305 310 315 320

Asp Val Asn Ala Pro Asp Ala Gly Gln Tyr Ser Gly Gln Ile Tyr Ile  
 325 330 335

Thr Phe Thr Pro Ser Val Glu Asn Leu  
 340 345

&lt;210&gt; SEQ ID NO 96

&lt;211&gt; LENGTH: 143

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Escherichia coli

&lt;400&gt; SEQUENCE: 96

Val Glu Lys Asn Ile Thr Val Arg Ala Ser Val Asp Pro Lys Leu Asp  
 1 5 10 15

Leu Leu Gln Ala Asp Gly Thr Ser Leu Pro Asp Ser Ile Ala Leu Thr  
 20 25 30

Tyr Ser Ser Ala Ser Asn Asn Phe Glu Val Tyr Ser Leu Asn Thr Ala  
 35 40 45

Ile His Thr Asn Asp Lys Thr Lys Ala Val Val Val Lys Leu Ser Ala  
 50 55 60

Pro Ala Val Leu Ser Asn Ile Met Lys Pro Ser Ser Gln Ile Pro Met  
 65 70 75 80

Lys Val Thr Leu Gly Lys Thr Leu Ser Thr Ala Asp Ala Glu Phe  
 85 90 95

Ala Ala Asp Thr Leu Asn Phe Gly Ala Ser Gly Val Glu Asn Val Ser  
 100 105 110

Ser Val Gln Gln Leu Thr Ile His Ala Glu Ala Ala Pro Pro Glu Ala



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<210> SEQ ID NO 98
<211> LENGTH: 147
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 98
Val Glu Lys Thr Ile Ser Val Thr Ala Ser Val Asp Pro Thr Val Asp
1          5          10          15
Leu Leu Gln Ser Asp Gly Ser Ala Leu Pro Asn Ser Val Ala Leu Thr
20          25          30
Tyr Ser Pro Ala Val Gly Gly Phe Glu Ala His Thr Ile Asn Thr Val
35          40          45
Val His Thr Asn Asp Pro Ala Lys Gly Val Ile Val Lys Leu Ser Ala
50          55          60
Glu Pro Val Leu Ser Asn Val Leu Asn Pro Thr Leu Gln Ile Pro Val
65          70          75          80
Ser Val Asn Phe Ala Gly Lys Lys Leu Thr Thr Thr Gly Thr Thr Ile
85          90          95
Glu Ser Asn Lys Leu Asn Phe Ala Ser Ser Gly Val Asp Lys Val Ser
100         105         110
Ser Thr Gln Lys Leu Ser Ile His Ala Asp Thr Thr Gln Val Thr Gly
115        120        125
Gly Leu Thr Ala Gly Gln Tyr Gln Gly Leu Val Ser Ile Ile Leu Thr
130        135        140

Gln Ser Thr
145

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<210> SEQ ID NO 99
<211> LENGTH: 146
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 99
Ala Ala Gly Pro Thr Leu Thr Lys Glu Leu Ala Leu Asn Val Leu Ser
1          5          10          15
Pro Ala Ala Leu Asp Ala Thr Trp Ala Pro Gln Asp Asn Leu Thr Leu
20          25          30
Ser Asn Thr Gly Val Ser Asn Thr Leu Val Gly Val Leu Thr Leu Ser
35          40          45
Asn Thr Ser Ile Asp Thr Val Ser Ile Ala Ser Thr Asn Val Ser Asp
50          55          60
Thr Ser Lys Asn Gly Thr Val Thr Phe Ala His Glu Thr Asn Asn Ser
65          70          75          80
Ala Ser Phe Ala Thr Thr Ile Ser Thr Asp Asn Ala Asn Ile Thr Leu
85          90          95
Asp Lys Asn Ala Gly Asn Thr Ile Val Lys Thr Thr Asn Gly Ser Gln
100         105         110
Leu Pro Thr Asn Leu Pro Leu Lys Phe Ile Thr Thr Glu Gly Asn Glu
115        120        125
His Leu Val Ser Gly Asn Tyr Arg Ala Asn Ile Thr Ile Thr Ser Thr
130        135        140

Ile Lys
145

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<210> SEQ ID NO 100
<211> LENGTH: 143

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<212> TYPE: PRT  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 100

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Ala Val Gly Pro Thr Lys Asp Met Ser Leu Gly Ala Asn Leu Thr Ser
1           5           10           15
Glu Pro Thr Leu Ala Ile Asp Phe Thr Pro Ile Glu Asn Ile Tyr Val
20           25           30
Gly Ala Asn Tyr Gly Lys Asp Ile Gly Thr Leu Val Phe Thr Thr Asn
35           40           45
Asp Leu Thr Asp Ile Thr Leu Met Ser Ser Arg Ser Val Val Asp Gly
50           55           60
Arg Gln Thr Gly Phe Phe Thr Phe Met Asp Ser Ser Ala Thr Tyr Lys
65           70           75           80
Ile Ser Thr Lys Leu Gly Ser Ser Asn Asp Val Asn Ile Gln Glu Ile
85           90           95
Thr Gln Gly Ala Lys Ile Thr Pro Val Ser Gly Glu Lys Thr Leu Pro
100          105          110
Lys Lys Phe Thr Leu Lys Leu His Ala His Arg Ser Ser Ser Thr Val
115          120          125
Pro Gly Thr Tyr Thr Val Gly Leu Asn Val Thr Ser Asn Val Ile
130          135          140
    
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<210> SEQ ID NO 101  
 <211> LENGTH: 1836  
 <212> TYPE: DNA  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 101

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atgagaacag aaatagcgac taaaaacttc ccagtatcaa cgactatttc aaaaagtgtt 60
tttgcacctg aaccacgaat acagccttct tttggtgaaa atgttggaag ggaaggagct 120
ttattattta gtgtgaactt aactgttcct gaaaatgtat cccaggtaac ggtctaccct 180
gtttatgatg aagattatgg gttaggacga ctagttaaata ccgctgatgc ttccaatca 240
ataatctacc agattgttga tgagaaaggg aaaaaaatgt taaaagatca tgggtgcagag 300
gttacaccta atcaacaat aacttttaaa gcgctgaatt atactagcgg ggaaaaaaaa 360
atatctcctg gaatatataa cgatcagggt atggttggtt actacgtcaa cgacaataaa 420
caaggaaact ggcaatataa atctctggat gtaaatgtaa atattgagca aaattttatt 480
ccagatattg attccgctgt tcgtataata cctgttaatt acgattcggg cccgaaactg 540
gattcacagt tatatacggg tgagatgacg atccctgcag gtgtaagcgc agttaaatac 600
gcaccaacag atagtctgac atcttctgga cagcagatcg gaaagctggt taatgtaaac 660
aatccagatc aaaatatgaa ttattatatac agaaaggatt ctggcgctgg taactttatg 720
gcaggacaaa aaggatcctt tctgtcaaaa gagaatacgt catacacatt ctcagcaatt 780
tatactggtg gcgaataacc taatagcgga tattcgtctg gtacttatgc aggaaatttg 840
actgtatcat tttacagcaa tgacaataaa caaagaacag aaatagcgac taaaaacttc 900
ccagtatcca cgactatttc aggcacatta gctattgatt ttacgcctat tgaaaatatt 960
tatgtaggty ccaattatgg taaagatatt ggaacccttg tttcacaac aaatgattta 1020
acagatatta cattgatgtc atctcgcagc gttgttgatg gtcgccagac tggttttttt 1080
accttcatgg actcatcagc cacttacaaa attagtacaa aactgggatc atcgaatgat 1140
gtaaaccattc aagaatttac tcaaggagct aaaattactc ctgttagtgg agagaaaact 1200
    
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ttgcctaaaa aattcactct taagctacat gcacacagga gtagcagtac agttccaggt 1260
acgtatactg ttggtcttaa cgtaaccagt aacgttattg ataacaagca ggcagcgggg 1320
cccactctaa ccaagaact ggcattaaat gtgctttctc ctgcagctct ggatgcaact 1380
tgggctcttc aggataattht aacattatcc aatactggcg tttctaatac tttggtggg 1440
gttttgactc tttcaaatac cagtattgat acagttagca ttgtagctac aaatgtttct 1500
gatacatcta agaatgggtac agtaactttt gcacatgaga caaataactc tgctagcttt 1560
gccaccacca tttcaacaga taatgccaac attacgttgg ataaaaatgc tggaaatagc 1620
attgttaaaa ctacaaatgg gagtcagttg ccaactaatt taccacttaa gtttattacc 1680
actgaaggta acgaacattht agtttcaggt aattaccgtg caaatataac aattacttgc 1740
acaattaagc ataacaagca ggcggcaggt ccaaccctga ctaaggagtt agcgctgaac 1800
gttctgagcc tcgagcacca ccaccaccac cactga 1836

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&lt;210&gt; SEQ ID NO 102

&lt;211&gt; LENGTH: 611

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Escherichia coli

&lt;400&gt; SEQUENCE: 102

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Met Arg Thr Glu Ile Ala Thr Lys Asn Phe Pro Val Ser Thr Thr Ile
 1           5           10          15
Ser Lys Ser Phe Phe Ala Pro Glu Pro Arg Ile Gln Pro Ser Phe Gly
          20           25          30
Glu Asn Val Gly Lys Glu Gly Ala Leu Leu Phe Ser Val Asn Leu Thr
          35           40          45
Val Pro Glu Asn Val Ser Gln Val Thr Val Tyr Pro Val Tyr Asp Glu
          50           55          60
Asp Tyr Gly Leu Gly Arg Leu Val Asn Thr Ala Asp Ala Ser Gln Ser
 65           70           75          80
Ile Ile Tyr Gln Ile Val Asp Glu Lys Gly Lys Lys Met Leu Lys Asp
          85           90          95
His Gly Ala Glu Val Thr Pro Asn Gln Gln Ile Thr Phe Lys Ala Leu
          100          105          110
Asn Tyr Thr Ser Gly Glu Lys Lys Ile Ser Pro Gly Ile Tyr Asn Asp
          115          120          125
Gln Val Met Val Gly Tyr Tyr Val Asn Asp Asn Lys Gln Gly Asn Trp
          130          135          140
Gln Tyr Lys Ser Leu Asp Val Asn Val Asn Ile Glu Gln Asn Phe Ile
          145          150          155          160
Pro Asp Ile Asp Ser Ala Val Arg Ile Ile Pro Val Asn Tyr Asp Ser
          165          170          175
Asp Pro Lys Leu Asp Ser Gln Leu Tyr Thr Val Glu Met Thr Ile Pro
          180          185          190
Ala Gly Val Ser Ala Val Lys Ile Ala Pro Thr Asp Ser Leu Thr Ser
          195          200          205
Ser Gly Gln Gln Ile Gly Lys Leu Val Asn Val Asn Asn Pro Asp Gln
          210          215          220
Asn Met Asn Tyr Tyr Ile Arg Lys Asp Ser Gly Ala Gly Asn Phe Met
          225          230          235          240
Ala Gly Gln Lys Gly Ser Phe Pro Val Lys Glu Asn Thr Ser Tyr Thr
          245          250          255

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gtatcggcag ataaaaatcc cggaagtga aacatgacta atactattgg tccccatgac	120
aggggggggat cttcccccat atataatc ttaaattcct atcttacagc atacaatgga	180
agccatcadc tgtatgatag gatgagtttt ttatgttgt cttctcaaaa tacactgaat	240
ggagcatgcc caagcagtga tgcccctggc actgctacaa ttgatggcga aacaaatata	300
acattacaat ttacggaaaa aagaagtcta attaaaagag aactgcaaat taaaggctat	360
aaacaatttt tgttcaaaaa tgctaattgc ccatetaaac tagcacttaa ctcatctcat	420
tttcaatgta atagagaaca agcttcaggt gctactttat cgttatacat accagctggt	480
gaattaaata aattaccctt tgggggggtc tgggaatgcc ttctgaagct aaatgtaaaa	540
agacgatatg atacaaccta tgggacttac actataaaca tcacagttaa tttactgat	600
aagggaaata ttcagatag gttaccacag ttcaaaagta acgctcgtgt cgatctaac	660
ttgctccaa ctgggtgggg tacatatatc ggaagaaatt ctgttgatg gtgcttttat	720
gatggatata gtactaacag cagctcttta gagataagat ttcaggatga taattctaaa	780
tctgatggaa aattttatct aaagaaaata aatgatgact ccaaagaact tgtatacact	840
ttgtcacttc tcctggcagg taaaaattta acaccaaaa atggacaggc attaaatatt	900
aacctgctt ctctggaac aaactggaat agaattacag ctgtcccat gccagaaatc	960
agtgttccgg tgtgtgttg gcctggacgt ttgcaattgg atgcaaaagt gaaaaatccc	1020
gaggctggac aatatatggg gaatattaaa attacttca caccaagtag tcaaacactc	1080
gacaataaac aagtagagaa aaatattact gtaacagcta gtgttgatc tgcaattgat	1140
cttttgcaag ctgatggcaa tgctctgcca tcagctgtaa agttagctta ttctccgca	1200
tcaaaaactt ttgaaagtta cagagtaatg actcaagttc atacaaaaga tgcaactaaa	1260
aaagtaattg ttaaacttgc tgatacacca cagcttacag atgttctgaa ttaactggt	1320
caaatgccta tcagtgtgtc atggggagga caagtattat ctacaacagc caaagaattt	1380
gaagctgctg ctttgggata ttctgcatc ggtgtaaatg gcgtatcadc ttctcaagag	1440
ttagtaatta gcgctgcacc taaaactgcc ggtaccgccc caactgcagg aaactattca	1500
ggagtagtat ctcttgaat gactttggga tccgacaata aacaagtaga gaaaaatatt	1560
actgtaacag ctagtgtoga cctactatt gatattcttc aagcaaatgg ttctgcgcta	1620
ccgacagctg tagatttaac ttatctacct ggtgcaaaaa cttttgaaaa ttacagtgtt	1680
ctaaccaga tttacacaaa tgaccctca aaaggtttag atgttcgact ggtgataca	1740
ccgaaactta caaatatttt gcaaccgaca tctaccatc ctcttactgt ctcatgggca	1800
gggaagacat taagtacaag tgcctcagaag attgcagttg gcgatctggg ttttggttcc	1860
accggaacgg caggtgttcc gaatagtaaa gaattagtaa ttggagcaac tacatccgga	1920
actgcaccaa gtgcaggtaa gtatcaaggc gtcgtttcca ttgtaatgac tcaatcgacc	1980
gacacagccg cgctgttcc tgacaataaa caagtagaga aaaatattac tgtgacagcc	2040
agtgttgatc ctactattga cattttgcaa gctgatggta gtagtttacc tactgctgta	2100
gaattaaact attcacctgc ggcaagtcgt tttgaaaatt ataaaatcgc aactaaagt	2160
catacaaatg ttataaataa aaatgtacta gttaagcttg taaatgatcc aaaacttaca	2220
aatgttttgg attctacaaa acaactcccc attactgtat catatggagg aaagactcta	2280
tcaaccgcag atgtgacttt tgaacctgca gaattaaatt ttggaacgctc aggtgtaact	2340
ggtgtatctt cttccaaga tttagtgatt ggtgcgacta cagcacaagc accaacggcg	2400
ggaaattata gtggggtcgt ttctatctta atgacctag catcagacaa taaacaagt	2460

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gaaaaaata tcaactgtaac agctagtggtt gatcctacgc tcgagcacca ccaccaccac 2520

cactga 2526

<210> SEQ ID NO 104

<211> LENGTH: 841

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 104

Met Asn Lys Ile Leu Phe Ile Phe Thr Leu Phe Phe Ser Ser Gly Phe  
1 5 10 15

Phe Thr Phe Ala Val Ser Ala Asp Lys Asn Pro Gly Ser Glu Asn Met  
20 25 30

Thr Asn Thr Ile Gly Pro His Asp Arg Gly Gly Ser Ser Pro Ile Tyr  
35 40 45

Asn Ile Leu Asn Ser Tyr Leu Thr Ala Tyr Asn Gly Ser His His Leu  
50 55 60

Tyr Asp Arg Met Ser Phe Leu Cys Leu Ser Ser Gln Asn Thr Leu Asn  
65 70 75 80

Gly Ala Cys Pro Ser Ser Asp Ala Pro Gly Thr Ala Thr Ile Asp Gly  
85 90 95

Glu Thr Asn Ile Thr Leu Gln Phe Thr Glu Lys Arg Ser Leu Ile Lys  
100 105 110

Arg Glu Leu Gln Ile Lys Gly Tyr Lys Gln Phe Leu Phe Lys Asn Ala  
115 120 125

Asn Cys Pro Ser Lys Leu Ala Leu Asn Ser Ser His Phe Gln Cys Asn  
130 135 140

Arg Glu Gln Ala Ser Gly Ala Thr Leu Ser Leu Tyr Ile Pro Ala Gly  
145 150 155 160

Glu Leu Asn Lys Leu Pro Phe Gly Gly Val Trp Asn Ala Val Leu Lys  
165 170 175

Leu Asn Val Lys Arg Arg Tyr Asp Thr Thr Tyr Gly Thr Tyr Thr Ile  
180 185 190

Asn Ile Thr Val Asn Leu Thr Asp Lys Gly Asn Ile Gln Ile Trp Leu  
195 200 205

Pro Gln Phe Lys Ser Asn Ala Arg Val Asp Leu Asn Leu Arg Pro Thr  
210 215 220

Gly Gly Gly Thr Tyr Ile Gly Arg Asn Ser Val Asp Met Cys Phe Tyr  
225 230 235 240

Asp Gly Tyr Ser Thr Asn Ser Ser Ser Leu Glu Ile Arg Phe Gln Asp  
245 250 255

Asp Asn Ser Lys Ser Asp Gly Lys Phe Tyr Leu Lys Lys Ile Asn Asp  
260 265 270

Asp Ser Lys Glu Leu Val Tyr Thr Leu Ser Leu Leu Leu Ala Gly Lys  
275 280 285

Asn Leu Thr Pro Thr Asn Gly Gln Ala Leu Asn Ile Asn Thr Ala Ser  
290 295 300

Leu Glu Thr Asn Trp Asn Arg Ile Thr Ala Val Thr Met Pro Glu Ile  
305 310 315 320

Ser Val Pro Val Leu Cys Trp Pro Gly Arg Leu Gln Leu Asp Ala Lys  
325 330 335

Val Lys Asn Pro Glu Ala Gly Gln Tyr Met Gly Asn Ile Lys Ile Thr  
340 345 350



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770	775	780
Ser Gln Asp Leu Val Ile Gly Ala Thr Thr Ala Gln Ala Pro Thr Ala		
785	790	795 800
Gly Asn Tyr Ser Gly Val Val Ser Ile Leu Met Thr Leu Ala Ser Asp		
	805	810 815
Asn Lys Gln Val Glu Lys Asn Ile Thr Val Thr Ala Ser Val Asp Pro		
	820	825 830
Thr Leu Glu His His His His His His		
	835	840

<210> SEQ ID NO 105  
 <211> LENGTH: 2164  
 <212> TYPE: DNA  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 105

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atgaaaaaga tatttatttt ttgtctatc atattttctg cggtggtcag tgcggggcga    60
tacccgaaaa ctacagtagg taactctgacg aagagttttc aagcccctcg tcaggataga    120
agcgtacaat caccaatata taacatcttt acgaatcatg tggctggata tagtttgagt    180
cataacttat atgacaggat tgttttttta tgtacatcct cgtcgaatcc ggttaatggt    240
gcttgcccaa ccattggaac atctggagtt caatacggta ctacaacat aaccttgcat    300
tttacagaaa aaagaagtct gataaaaaa aatattaatc ttgcaggtaa taagaaacca    360
atatgggaga atcagagttg cgacactagc aatctaattg tgttgaatc gaagtcttgg    420
tcctgtgggg cttacggaaa tgctaocgga acacttctaa atctgtatat ccctgcagga    480
gaaatcaaca aattgccttt tggagggata tgggaggcaa ctctgatctt acgcttatca    540
agatatggcg aagtcagtag caccattac ggcaattata ccgtaaatat tacggttgat    600
ttaactgata aaggaatat tcaggtatgg cttccagggt ttcacagcaa cccgcgtgta    660
gacctgaatc tgcaccctat cgtaattat aaatatagtg gtagtaatc actcgacatg    720
tgtttctatg atggatatag taaaaacagt gatagcatgg taataaagt ccaggatgat    780
aatcctacct attcatctga atataactt tataagatag ggggcaactga aaaattacc    840
tatgtgtttt cactgcttat gggagaaaa atattttatc cagtgaatgg tcaatcatt    900
actatcaatg acagtagtgt actcgaaca aactggaatc gagtaaccgc agttgctatg    960
ccggaagtta atgttccagt attatgctgg ccagcaagat tgctattaaa tgctgatgta   1020
aatgtcctcg atgcaggaca gtattcagga cagatatata taacatttac acccagtgtc   1080
gaaaatttag gcggtggagt cgaaaaaaat attactgtga gggcaagtgt tgaccctaaa   1140
cttgatcttc tgcaagcaga tggaacttca ctgccggact ctatgcatt aacctattct   1200
tcggcttcaa ataatttga agtttactct cttaatactg ctattcatac aaatgacaaa   1260
agcaagggag ttgtagttaa gctgtcagct tcaccagttc tgtccaatat tatgaagcca   1320
aactcgaaaa ttccgatgaa agtgactttg ggggggaaga cgctgaatac aactgatact   1380
gagtttactg ttgatactct gaactttggt acatctggtg ttgaaaacgt ttcttccact   1440
caacagctta cgattcatgc agacacacaa ggaactgcgc ctgaggcagg caattaccaa   1500
ggtattatct ctcttatcat gactcaaaaa acagggggcg gtgtcgaaaa aaatattact   1560
gtgagggcaa gtgtcgaccc taaacttgac cttctgcaat ctgatggctc tgcgctgccg   1620
aactctgtcg cattaaccta ttctccgct gtaaataatt ttgaagctca caccatcaac   1680
accgttgttc atacaatga ctcagataaa ggtgtgtgtg tgaagctgct agcagatcca   1740
    
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gtcctgtcca atgttctgaa tccaacctg caaatctctg tttctgtgaa tttcgcagga 1800
aaaccactga gcacaacagg cattaccatc gactccaatg atctgaactt tgcttcgagt 1860
ggtgttaata aagtttcttc tacgcagaaa ctttcaatcc atgcagatgc tactcgggta 1920
actggcggcg cactaacagc tggtaatat cagggactcg tatcaattat cctgactaag 1980
tcaacggggg gcggtgtcga gaagaccatt agcgttacgg cgagtgttga cccgacgggc 2040
acattagcta ttgattttac gcctattgaa aatatttatg taggtgccaa ttatggtaaa 2100
gatattggaa cccttgtttt cacaacaaat gatttaactc gagcaccacc accaccacca 2160
ctga 2164

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&lt;210&gt; SEQ ID NO 106

&lt;211&gt; LENGTH: 687

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Escherichia coli

&lt;400&gt; SEQUENCE: 106

```

Met Lys Lys Ile Phe Ile Phe Leu Ser Ile Ile Phe Ser Ala Val Val
 1          5          10          15
Ser Ala Gly Arg Tyr Pro Glu Thr Thr Val Gly Asn Leu Thr Lys Ser
 20          25          30
Phe Gln Ala Pro Arg Gln Asp Arg Ser Val Gln Ser Pro Ile Tyr Asn
 35          40          45
Ile Phe Thr Asn His Val Ala Gly Tyr Ser Leu Ser His Asn Leu Tyr
 50          55          60
Asp Arg Ile Val Phe Leu Cys Thr Ser Ser Ser Asn Pro Val Asn Gly
 65          70          75          80
Ala Cys Pro Thr Ile Gly Thr Ser Gly Val Gln Tyr Gly Thr Thr Thr
 85          90          95
Ile Thr Leu Gln Phe Thr Glu Lys Arg Ser Leu Ile Lys Arg Asn Ile
 100         105         110
Asn Leu Ala Gly Asn Lys Lys Pro Ile Trp Glu Asn Gln Ser Cys Asp
 115         120         125
Thr Ser Asn Leu Met Val Leu Asn Ser Lys Ser Trp Ser Cys Gly Ala
 130         135         140
Tyr Gly Asn Ala Asn Gly Thr Leu Leu Asn Leu Tyr Ile Pro Ala Gly
 145         150         155         160
Glu Ile Asn Lys Leu Pro Phe Gly Gly Ile Trp Glu Ala Thr Leu Ile
 165         170         175
Leu Arg Leu Ser Arg Tyr Gly Glu Val Ser Ser Thr His Tyr Gly Asn
 180         185         190
Tyr Thr Val Asn Ile Thr Val Asp Leu Thr Asp Lys Gly Asn Ile Gln
 195         200         205
Val Trp Leu Pro Gly Phe His Ser Asn Pro Arg Val Asp Leu Asn Leu
 210         215         220
His Pro Ile Gly Asn Tyr Lys Tyr Ser Gly Ser Asn Ser Leu Asp Met
 225         230         235         240
Cys Phe Tyr Asp Gly Tyr Ser Thr Asn Ser Asp Ser Met Val Ile Lys
 245         250         255
Phe Gln Asp Asp Asn Pro Thr Tyr Ser Ser Glu Tyr Asn Leu Tyr Lys
 260         265         270
Ile Gly Gly Thr Glu Lys Leu Pro Tyr Ala Val Ser Leu Leu Met Gly
 275         280         285

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Glu Lys Ile Phe Tyr Pro Val Asn Gly Gln Ser Phe Thr Ile Asn Asp  
 290 295 300  
 Ser Ser Val Leu Glu Thr Asn Trp Asn Arg Val Thr Ala Val Ala Met  
 305 310 315 320  
 Pro Glu Val Asn Val Pro Val Leu Cys Trp Pro Ala Arg Leu Leu Leu  
 325 330 335  
 Asn Ala Asp Val Asn Ala Pro Asp Ala Gly Gln Tyr Ser Gly Gln Ile  
 340 345 350  
 Tyr Ile Thr Phe Thr Pro Ser Val Glu Asn Leu Gly Gly Gly Val Glu  
 355 360 365  
 Lys Asn Ile Thr Val Arg Ala Ser Val Asp Pro Lys Leu Asp Leu Leu  
 370 375 380  
 Gln Ala Asp Gly Thr Ser Leu Pro Asp Ser Ile Ala Leu Thr Tyr Ser  
 385 390 395 400  
 Ser Ala Ser Asn Asn Phe Glu Val Tyr Ser Leu Asn Thr Ala Ile His  
 405 410 415  
 Thr Asn Asp Lys Ser Lys Gly Val Val Val Lys Leu Ser Ala Ser Pro  
 420 425 430  
 Val Leu Ser Asn Ile Met Lys Pro Asn Ser Gln Ile Pro Met Lys Val  
 435 440 445  
 Thr Leu Gly Gly Lys Thr Leu Asn Thr Thr Asp Thr Glu Phe Thr Val  
 450 455 460  
 Asp Thr Leu Asn Phe Gly Thr Ser Gly Val Glu Asn Val Ser Ser Thr  
 465 470 475 480  
 Gln Gln Leu Thr Ile His Ala Asp Thr Gln Gly Thr Ala Pro Glu Ala  
 485 490 495  
 Gly Asn Tyr Gln Gly Ile Ile Ser Leu Ile Met Thr Gln Lys Thr Gly  
 500 505 510  
 Gly Gly Val Glu Lys Asn Ile Thr Val Arg Ala Ser Val Asp Pro Lys  
 515 520 525  
 Leu Asp Leu Leu Gln Ser Asp Gly Ser Ala Leu Pro Asn Ser Val Ala  
 530 535 540  
 Leu Thr Tyr Ser Pro Ala Val Asn Asn Phe Glu Ala His Thr Ile Asn  
 545 550 555 560  
 Thr Val Val His Thr Asn Asp Ser Asp Lys Gly Val Val Val Lys Leu  
 565 570 575  
 Ser Ala Asp Pro Val Leu Ser Asn Val Leu Asn Pro Thr Leu Gln Ile  
 580 585 590  
 Pro Val Ser Val Asn Phe Ala Gly Lys Pro Leu Ser Thr Thr Gly Ile  
 595 600 605  
 Thr Ile Asp Ser Asn Asp Leu Asn Phe Ala Ser Ser Gly Val Asn Lys  
 610 615 620  
 Val Ser Ser Thr Gln Lys Leu Ser Ile His Ala Asp Ala Thr Arg Val  
 625 630 635 640  
 Thr Gly Gly Ala Leu Thr Ala Gly Gln Tyr Gln Gly Leu Val Ser Ile  
 645 650 655  
 Ile Leu Thr Lys Ser Thr Gly Gly Gly Val Glu Lys Thr Ile Ser Val  
 660 665 670  
 Thr Ala Ser Val Asp Pro Thr Leu Glu His His His His His His  
 675 680 685

&lt;210&gt; SEQ ID NO 107

&lt;211&gt; LENGTH: 2278

&lt;212&gt; TYPE: DNA

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&lt;213&gt; ORGANISM: Escherichia coli

&lt;400&gt; SEQUENCE: 107

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atgaaaaaga tatttatttt tttgtctatc atattttctg cggtggtcag tgccgggcca    60
tacccgaaaa ctacagtagg taatctgacg aagagttttc aagcccctcg tcaggataga    120
agcgtacaat caccaatata taacatcttt acgaatcatg tggctggata tagtttgagt    180
cataacttat atgacaggat tgttttttta tgtacatcct cgtcgaatcc ggttaatggt    240
gcttgcccaa ccattggaac atctggagtt caatacggta ctacaacat aaccttgca    300
tttacagaaa aaagaagtct gataaaaaa aatattaatc ttgcaggtaa taagaaacca    360
atatgggaga atcagagttg cgacactagc aatctaattg tggttgaatc gaagtcttgg    420
tcctgtgggg cttacggaaa tgctaocgga acacttctaa atctgtatat cctgcagga    480
gaaatcaaca aattgccttt tggagggata tgggaggcaa ctctgatctt acgcttatca    540
agatatggcg aagtcagtag caccattac ggcaattata ccgtaaatat tacggttgat    600
ttaactgata aaggaatat tcaggtatgg cttccagggt ttcacagcaa cccgcgtgta    660
gacctgaatc tgcaccctat cggttaattat aaatatagtg gtagtaatc actcgacatg    720
tgtttctatg atggatatag taaaaacagt gatagcatgg taataaagt ccaggatgat    780
aatcctacct attcatctga atataatctt tataagatag ggggcaactga aaaattacc    840
tatgtgtttt cactgcttat gggagaaaa atattttatc cagtgaatgg tcaatcattt    900
actatcaatg acagtagtgt actcgaaaca aactggaatc gagtaaccgc agttgctatg    960
ccggaagtta atgttccagt attatgctgg ccagcaagat tgctattaaa tgctgatgta   1020
aatgtcccg atgcaggaca gtattcagga cagatatata taacatttac acccagtgtc   1080
gaaaatttag gcggtggagt cgaaaaaat attactgtga gggcaagtgt tgaccctaaa   1140
cttgatcttc tgcaagcaga tggaaactca ctgccggact ctatgcatt aacctattct   1200
tcggcttcaa ataatttga agtttactct ctttaactg ctattcatac aaatgacaaa   1260
agcaagggag ttgtagttaa gctgtcagct tcaccagttc tgtccaatat tatgaagcca   1320
aactcgaaa tccgatgaa agtgactttg ggggggaaga cgctgaatac aactgatact   1380
gagtttactg ttgatactct gaactttggt acatctggtg ttgaaaactg ttcttccact   1440
caacagctta cgattcatgc agacacacaa ggaactgcgc ctgaggcagg caattaccaa   1500
ggtattatth ctcttacoat gactcaaaaa acagggggcg gtgtcgaaaa aaatattact   1560
gtgagggcaa gtgtcgaccc taaacttaaa ctaaagaaaa caattggcgc aatggctctg   1620
gcgacattat ttgcaactat gggagcatct gcggtcgaga agaccattag cgttacggcg   1680
agtgttgacc cgactgttga ccttctgcaa tctgatggct ctgcgctgcc gaactctgtc   1740
gcattaacct attctccggc tgtaaataat tttgaagctc acaccatcaa caccgttgtt   1800
catacaaatg actcagataa aggtgttgtt gtgaagctgt cagcagatcc agtctgttcc   1860
aatgttctga atccaacct gcaaattcct gtttctgtga atttcgagg aaaaccactg   1920
agcacaacag gcattacat cgactccaat gatctgaact ttgcttcgag tgggtgtaat   1980
aaagtttctt ctacgcagaa actttcaatc catgcagatg ctactcgggt aactggcggc   2040
gcactaacag ctggtcaata tcagggactc gtatcaatta tcctgactaa gtcacagtaa   2100
gggggcggtg tcgagaagac cattagcgtt acggcgagtg ttgacccgac gggcacatta   2160
gctattgatt ttacgcctat tgaaaatatt tatgtagggtg ccaattatgg taaagatatt   2220
ggaacccttg tttcacaac aaatgattta actcgagcac caccaccacc accactga   2278

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<210> SEQ ID NO 108  
 <211> LENGTH: 703  
 <212> TYPE: PRT  
 <213> ORGANISM: Escherichia coli  
  
 <400> SEQUENCE: 108  
  
 Met Lys Lys Ile Phe Ile Phe Leu Ser Ile Ile Phe Ser Ala Val Val  
 1 5 10 15  
  
 Ser Ala Gly Arg Tyr Pro Glu Thr Thr Val Gly Asn Leu Thr Lys Ser  
 20 25 30  
  
 Phe Gln Ala Pro Arg Gln Asp Arg Ser Val Gln Ser Pro Ile Tyr Asn  
 35 40 45  
  
 Ile Phe Thr Asn His Val Ala Gly Tyr Ser Leu Ser His Asn Leu Tyr  
 50 55 60  
  
 Asp Arg Ile Val Phe Leu Cys Thr Ser Ser Ser Asn Pro Val Asn Gly  
 65 70 75 80  
  
 Ala Cys Pro Thr Ile Gly Thr Ser Gly Val Gln Tyr Gly Thr Thr Thr  
 85 90 95  
  
 Ile Thr Leu Gln Phe Thr Glu Lys Arg Ser Leu Ile Lys Arg Asn Ile  
 100 105 110  
  
 Asn Leu Ala Gly Asn Lys Lys Pro Ile Trp Glu Asn Gln Ser Cys Asp  
 115 120 125  
  
 Thr Ser Asn Leu Met Val Leu Asn Ser Lys Ser Trp Ser Cys Gly Ala  
 130 135 140  
  
 Tyr Gly Asn Ala Asn Gly Thr Leu Leu Asn Leu Tyr Ile Pro Ala Gly  
 145 150 155 160  
  
 Glu Ile Asn Lys Leu Pro Phe Gly Gly Ile Trp Glu Ala Thr Leu Ile  
 165 170 175  
  
 Leu Arg Leu Ser Arg Tyr Gly Glu Val Ser Ser Thr His Tyr Gly Asn  
 180 185 190  
  
 Tyr Thr Val Asn Ile Thr Val Asp Leu Thr Asp Lys Gly Asn Ile Gln  
 195 200 205  
  
 Val Trp Leu Pro Gly Phe His Ser Asn Pro Arg Val Asp Leu Asn Leu  
 210 215 220  
  
 His Pro Ile Gly Asn Tyr Lys Tyr Ser Gly Ser Asn Ser Leu Asp Met  
 225 230 235 240  
  
 Cys Phe Tyr Asp Gly Tyr Ser Thr Asn Ser Asp Ser Met Val Ile Lys  
 245 250 255  
  
 Phe Gln Asp Asp Asn Pro Thr Tyr Ser Ser Glu Tyr Asn Leu Tyr Lys  
 260 265 270  
  
 Ile Gly Gly Thr Glu Lys Leu Pro Tyr Ala Val Ser Leu Leu Met Gly  
 275 280 285  
  
 Glu Lys Ile Phe Tyr Pro Val Asn Gly Gln Ser Phe Thr Ile Asn Asp  
 290 295 300  
  
 Ser Ser Val Leu Glu Thr Asn Trp Asn Arg Val Thr Ala Val Ala Met  
 305 310 315 320  
  
 Pro Glu Val Asn Val Pro Val Leu Cys Trp Pro Ala Arg Leu Leu Leu  
 325 330 335  
  
 Asn Ala Asp Val Asn Ala Pro Asp Ala Gly Gln Tyr Ser Gly Gln Ile  
 340 345 350  
  
 Tyr Ile Thr Phe Thr Pro Ser Val Glu Asn Leu Gly Gly Gly Val Glu  
 355 360 365  
  
 Lys Asn Ile Thr Val Arg Ala Ser Val Asp Pro Lys Leu Asp Leu Leu

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370			375			380									
Gln	Ala	Asp	Gly	Thr	Ser	Leu	Pro	Asp	Ser	Ile	Ala	Leu	Thr	Tyr	Ser
385					390					395					400
Ser	Ala	Ser	Asn	Asn	Phe	Glu	Val	Tyr	Ser	Leu	Asn	Thr	Ala	Ile	His
				405						410					415
Thr	Asn	Asp	Lys	Ser	Lys	Gly	Val	Val	Val	Lys	Leu	Ser	Ala	Ser	Pro
			420							425				430	
Val	Leu	Ser	Asn	Ile	Met	Lys	Pro	Asn	Ser	Gln	Ile	Pro	Met	Lys	Val
		435						440						445	
Thr	Leu	Gly	Gly	Lys	Thr	Leu	Asn	Thr	Thr	Asp	Thr	Glu	Phe	Thr	Val
	450						455				460				
Asp	Thr	Leu	Asn	Phe	Gly	Thr	Ser	Gly	Val	Glu	Asn	Val	Ser	Ser	Thr
465				470						475					480
Gln	Gln	Leu	Thr	Ile	His	Ala	Asp	Thr	Gln	Gly	Thr	Ala	Pro	Glu	Ala
				485						490					495
Gly	Asn	Tyr	Gln	Gly	Ile	Ile	Ser	Leu	Ile	Met	Thr	Gln	Lys	Thr	Gly
		500						505						510	
Gly	Gly	Val	Glu	Lys	Asn	Ile	Thr	Val	Arg	Ala	Ser	Val	Asp	Pro	Lys
		515						520						525	
Leu	Asp	Val	Glu	Lys	Thr	Ile	Ser	Val	Thr	Ala	Ser	Val	Asp	Pro	Thr
	530						535				540				
Val	Asp	Leu	Leu	Gln	Ser	Asp	Gly	Ser	Ala	Leu	Pro	Asn	Ser	Val	Ala
545					550					555					560
Leu	Thr	Tyr	Ser	Pro	Ala	Val	Asn	Asn	Phe	Glu	Ala	His	Thr	Ile	Asn
				565						570					575
Thr	Val	Val	His	Thr	Asn	Asp	Ser	Asp	Lys	Gly	Val	Val	Val	Lys	Leu
			580					585						590	
Ser	Ala	Asp	Pro	Val	Leu	Ser	Asn	Val	Leu	Asn	Pro	Thr	Leu	Gln	Ile
		595						600						605	
Pro	Val	Ser	Val	Asn	Phe	Ala	Gly	Lys	Pro	Leu	Ser	Thr	Thr	Gly	Ile
	610				615						620				
Thr	Ile	Asp	Ser	Asn	Asp	Leu	Asn	Phe	Ala	Ser	Ser	Gly	Val	Asn	Lys
625					630					635					640
Val	Ser	Ser	Thr	Gln	Lys	Leu	Ser	Ile	His	Ala	Asp	Ala	Thr	Arg	Val
				645						650					655
Thr	Gly	Gly	Ala	Leu	Thr	Ala	Gly	Gln	Tyr	Gln	Gly	Leu	Val	Ser	Ile
			660					665						670	
Ile	Leu	Thr	Lys	Ser	Thr	Gly	Gly	Gly	Val	Glu	Lys	Thr	Ile	Ser	Val
		675						680						685	
Thr	Ala	Ser	Val	Asp	Pro	Thr	Leu	Glu	His	His	His	His	His	His	
	690						695				700				

&lt;210&gt; SEQ ID NO 109

&lt;211&gt; LENGTH: 1620

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Escherichia coli

&lt;400&gt; SEQUENCE: 109

```

atgaaaaaag tgatttttgt tttatccatg tttctatggt ctcagggtta cgggcaatca    60
tggcatacga acgtagagggc tggttcaata aataaaacag agtcgatagg ccccatagac    120
cgaagtgctg ctgcategta tctgtctcat tatatatttc atgaacatgt tgctgggttac    180
aataaagatc actctctttt tgacaggatg acgtttttat gtatgtcadc aacagatgca    240
tctaaagggtg catgtccgac aggagaaaac tccaaatcct ctcaagggga gactaatatt    300

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aagctaatat ttactgaaaa gaaaagtctg gccagaaaaa cattaaaactt aaaaggatat 360
aagagatfff tatatgaatc agatagatgc attcattatg tcgataaaat gaatctcaat 420
tctcactactg ttaaatgtgt aggttcattc acaagaggag tagatttcac tttatatatc 480
ccacaagggtg aaattgatgg gcttctaact ggaggtatat gggaggcaac actagagtta 540
cgagtcaaaa ggcattacga ctataatcat ggtacttaca aagttaatat cacagttgat 600
ttgacagaca aaggaaatat tcaggtctgg acaccaaagt ttcatagcga tcctagaatt 660
gatctgaatt tacgtcctga aggtaatggg aaatattctg gtagtaacgt gcttgagatg 720
tgtctctatg atggctatag tacacatagt caaagtatag aaatgaggtt tcaggatgac 780
tcacaaacag gaaataatga atataatctt ataaaaactg gagagccatt aaaaaaattg 840
ccatataaac tttctcttct tttaggagga cgagagtttt atccaaataa tggagaggtt 900
tttactatta atgatacttc gtcattgttt ataaactgga atcgtattaa gtctgtatcc 960
ttaccacaga ttagtattcc agtactatgc tggccagcaa acttgacatt tatgtcagag 1020
ctaaataatc cagaagcggg tgagtattca ggaatactta acgtaacatt tactcctagt 1080
agttcaagcc tagacaataa acaagccgag aaaaatatca ctgtaactgc tagcgttgat 1140
ccaactatcg atctgatgca atctgatggc acagcgttac caagtgcagt taatattgca 1200
tatcttccag gagagaaaag atttgaatct gctcgtatca ataccaagt tcataccaat 1260
aataaaacta agggatttca gataaagctt actaatgata atgtggtaat gactaactta 1320
tctgatccaa gcaagactat tcctttagag gtttcattcg ctggcactaa gctgagcaca 1380
gctgcaacat ctattactgc cgatcaatta aatgttggcg cagctggtgt agagacagtt 1440
tctgcaacta aggaactcgt tattaatgca ggaagcacc agcaactaa tattgtagct 1500
ggtaactatc aaggattggg gtcaattgtg cttactcaag aacctgacaa taaacaagcc 1560
gagaaaaata tcactgtaac tgctagcgtt gatccgacgc accaccacca ccaccactga 1620

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<210> SEQ ID NO 110
<211> LENGTH: 539
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

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<400> SEQUENCE: 110

```

Met Lys Lys Val Ile Phe Val Leu Ser Met Phe Leu Cys Ser Gln Val
1          5          10          15
Tyr Gly Gln Ser Trp His Thr Asn Val Glu Ala Gly Ser Ile Asn Lys
20        25        30
Thr Glu Ser Ile Gly Pro Ile Asp Arg Ser Ala Ala Ser Tyr Pro
35        40        45
Ala His Tyr Ile Phe His Glu His Val Ala Gly Tyr Asn Lys Asp His
50        55        60
Ser Leu Phe Asp Arg Met Thr Phe Leu Cys Met Ser Ser Thr Asp Ala
65        70        75        80
Ser Lys Gly Ala Cys Pro Thr Gly Glu Asn Ser Lys Ser Ser Gln Gly
85        90        95
Glu Thr Asn Ile Lys Leu Ile Phe Thr Glu Lys Lys Ser Leu Ala Arg
100       105       110
Lys Thr Leu Asn Leu Lys Gly Tyr Lys Arg Phe Leu Tyr Glu Ser Asp
115       120       125
Arg Cys Ile His Tyr Val Asp Lys Met Asn Leu Asn Ser His Thr Val
130       135       140

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Lys Cys Val Gly Ser Phe Thr Arg Gly Val Asp Phe Thr Leu Tyr Ile  
 145 150 155 160  
 Pro Gln Gly Glu Ile Asp Gly Leu Leu Thr Gly Gly Ile Trp Glu Ala  
 165 170 175  
 Thr Leu Glu Leu Arg Val Lys Arg His Tyr Asp Tyr Asn His Gly Thr  
 180 185 190  
 Tyr Lys Val Asn Ile Thr Val Asp Leu Thr Asp Lys Gly Asn Ile Gln  
 195 200 205  
 Val Trp Thr Pro Lys Phe His Ser Asp Pro Arg Ile Asp Leu Asn Leu  
 210 215 220  
 Arg Pro Glu Gly Asn Gly Lys Tyr Ser Gly Ser Asn Val Leu Glu Met  
 225 230 235 240  
 Cys Leu Tyr Asp Gly Tyr Ser Thr His Ser Gln Ser Ile Glu Met Arg  
 245 250 255  
 Phe Gln Asp Asp Ser Gln Thr Gly Asn Asn Glu Tyr Asn Leu Ile Lys  
 260 265 270  
 Thr Gly Glu Pro Leu Lys Lys Leu Pro Tyr Lys Leu Ser Leu Leu Leu  
 275 280 285  
 Gly Gly Arg Glu Phe Tyr Pro Asn Asn Gly Glu Ala Phe Thr Ile Asn  
 290 295 300  
 Asp Thr Ser Ser Leu Phe Ile Asn Trp Asn Arg Ile Lys Ser Val Ser  
 305 310 315 320  
 Leu Pro Gln Ile Ser Ile Pro Val Leu Cys Trp Pro Ala Asn Leu Thr  
 325 330 335  
 Phe Met Ser Glu Leu Asn Asn Pro Glu Ala Gly Glu Tyr Ser Gly Ile  
 340 345 350  
 Leu Asn Val Thr Phe Thr Pro Ser Ser Ser Ser Leu Asp Asn Lys Gln  
 355 360 365  
 Ala Glu Lys Asn Ile Thr Val Thr Ala Ser Val Asp Pro Thr Ile Asp  
 370 375 380  
 Leu Met Gln Ser Asp Gly Thr Ala Leu Pro Ser Ala Val Asn Ile Ala  
 385 390 395 400  
 Tyr Leu Pro Gly Glu Lys Arg Phe Glu Ser Ala Arg Ile Asn Thr Gln  
 405 410 415  
 Val His Thr Asn Asn Lys Thr Lys Gly Ile Gln Ile Lys Leu Thr Asn  
 420 425 430  
 Asp Asn Val Val Met Thr Asn Leu Ser Asp Pro Ser Lys Thr Ile Pro  
 435 440 445  
 Leu Glu Val Ser Phe Ala Gly Thr Lys Leu Ser Thr Ala Ala Thr Ser  
 450 455 460  
 Ile Thr Ala Asp Gln Leu Asn Phe Gly Ala Ala Gly Val Glu Thr Val  
 465 470 475 480  
 Ser Ala Thr Lys Glu Leu Val Ile Asn Ala Gly Ser Thr Gln Gln Thr  
 485 490 495  
 Asn Ile Val Ala Gly Asn Tyr Gln Gly Leu Val Ser Ile Val Leu Thr  
 500 505 510  
 Gln Glu Pro Asp Asn Lys Gln Ala Glu Lys Asn Ile Thr Val Thr Ala  
 515 520 525  
 Ser Val Asp Pro Thr His His His His His His  
 530 535

&lt;210&gt; SEQ ID NO 111

&lt;211&gt; LENGTH: 2490

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&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Escherichia coli

&lt;400&gt; SEQUENCE: 111

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atgaataaaa ttttatttat ttttacattg tttttttctt cagggttttt tacatttgcc      60
gtatcggcag ataaaaatcc cggaaagtga aacatgacta atactattgg tccccatgac      120
agggggggat cttcccccat atataatata ttaaattcct atcttacagc atacaatgga      180
agccatcatc tgtatgatag gatgagtttt ttatgtttgt cttctcaaaa tacactgaat      240
ggagcatgcc caagcagtga tgccccggc actgctacaa ttgatggcga aacaaatata      300
acattacaat ttacggaaaa aagaagtcta attaaaagag aactgcaaat taaaggctat      360
aaacaatttt tgttcaaaaa tgctaattgc ccatctaac tagcacttaa ctcatctcat      420
tttcaatgta atagagaaca agcttcaggt gctactttat cgttatacat accagctggt      480
gaattaaata aattaccttt tgggggggtc tggaaatgccc ttctgaagct aaatgtaaaa      540
agacgatatg atacaaccta tgggacttac actataaaca tcacagtaa tttactgat      600
aagggaataa ttcagatag gttaccacag ttcaaaagta acgctcgtgt cgatcttaac      660
ttgctccaa ctggtggtgg tacatatata ggaagaaatt ctgttgatat gtgcttttat      720
gatgatata gtactaacag cagctcttta gagataagat ttcaggatga taattctaaa      780
tctgatggaa aattttatct aaagaaaata aatgatgact ccaagaact tgtatacact      840
ttgtcacttc tcctggcagg taaaaattha acaccaacaa atggacaggc attaaatatt      900
aacactgctt ctctggaaac aaactggaat agaattacag ctgtcaccat gccagaaatc      960
agtgtccgg tgtgtgttg gctcggcagt ttgcaattgg atgcaaaagt gaaaaatccc     1020
gaggctggac aatataatgg gaatattaaa attactttca caccaagtag tcaaacactc     1080
gacaataaac aagtagagaa aaatattact gtaacagcta gtgttgatcc tgcaattgat     1140
cttttgcaag ctgatggcaa tgctctgcca tcagctgtaa agttagetta ttctcccgca     1200
tcaaaaactt ttgaaagtta cagagtaatg actcaagttc atacaaacga tgcaactaaa     1260
aaagtaattg ttaaaactgc tgatacacca cagcttacag atgttctgaa ttaactggt     1320
caaatgccta tcagtgtgtc atggggagga caagtattat ctacaacagc caaagaattt     1380
gaagctgctg ctttgggata ttctgcatcc ggtgtaaatg gcgtatcatc ttctcaagag     1440
ttagtaatta gcgctgcacc taaaactgcc ggtaccgccc caactgcagg aaactattca     1500
ggagtagtat ctcttgaat gactttggga tccgacaata aacaagtaga gaaaaatatt     1560
actgtaacag ctagtgtcga cctcgcaggg tcaaaaagtt ttttgcacc tgaaccacga     1620
atacagcctt cttttggtga aaatgttga aaggaaggag ctttattatt tagtgtgaac     1680
ttaactgttc ctgaaaatgt atcccaggta acggtctacc ctgtttatga tgaagattat     1740
gggttaggac gactagtaaa taccgctgat gcttcccaat caataatcta ccagattggt     1800
gatgaaaaag ggaaaaaaat gttaaaagat catggtgcag aggttacacc taatcaacaa     1860
ataactttta aagcgtgtaa ttatactagc ggggaaaaaa aaatatctcc tggaatatat     1920
aacgatcagg ttatggttgg ttactacgtc aacgacaata aacaaggaaa ctggcaatat     1980
aaatctctgg atgtaaatgt aaatattgag caaaatthta ttccagatat tgattccgct     2040
gttcgtataa tacctgttaa ttacgattcg gaccgaaac tggattcaca gttatatacg     2100
gttgagatga cgatccctgc aggtgtaagc gcagttaaaa tgcaccaac agatagtctg     2160
acatcttctg gacagcagat cggaaagctg gttaatgtaa acaatccaga tcaaaatatg     2220

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aattattata tcagaaagga ttctggcgct ggtaacttta tggcaggaca aaaaggatcc 2280
tttctgtca aagagaatac gtcatacaca ttctcagcaa tttatactgg tggcgaatac 2340
cctaatagcg gatattcgtc tggacttat gcaggaaatt tgactgtatc attttacagc 2400
aatgacaata aacaacgtac cgagattgcc accaagaatt ttccggtgag caccaccatc 2460
agcctcgagc accaccacca ccaccactga 2490

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&lt;210&gt; SEQ ID NO 112

&lt;211&gt; LENGTH: 829

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Escherichia coli

&lt;400&gt; SEQUENCE: 112

```

Met Asn Lys Ile Leu Phe Ile Phe Thr Leu Phe Phe Ser Ser Gly Phe
1          5          10          15
Phe Thr Phe Ala Val Ser Ala Asp Lys Asn Pro Gly Ser Glu Asn Met
20          25          30
Thr Asn Thr Ile Gly Pro His Asp Arg Gly Gly Ser Ser Pro Ile Tyr
35          40          45
Asn Ile Leu Asn Ser Tyr Leu Thr Ala Tyr Asn Gly Ser His His Leu
50          55          60
Tyr Asp Arg Met Ser Phe Leu Cys Leu Ser Ser Gln Asn Thr Leu Asn
65          70          75          80
Gly Ala Cys Pro Ser Ser Asp Ala Pro Gly Thr Ala Thr Ile Asp Gly
85          90          95
Glu Thr Asn Ile Thr Leu Gln Phe Thr Glu Lys Arg Ser Leu Ile Lys
100         105         110
Arg Glu Leu Gln Ile Lys Gly Tyr Lys Gln Phe Leu Phe Lys Asn Ala
115         120         125
Asn Cys Pro Ser Lys Leu Ala Leu Asn Ser Ser His Phe Gln Cys Asn
130         135         140
Arg Glu Gln Ala Ser Gly Ala Thr Leu Ser Leu Tyr Ile Pro Ala Gly
145         150         155         160
Glu Leu Asn Lys Leu Pro Phe Gly Gly Val Trp Asn Ala Val Leu Lys
165         170         175
Leu Asn Val Lys Arg Arg Tyr Asp Thr Thr Tyr Gly Thr Tyr Thr Ile
180         185         190
Asn Ile Thr Val Asn Leu Thr Asp Lys Gly Asn Ile Gln Ile Trp Leu
195         200         205
Pro Gln Phe Lys Ser Asn Ala Arg Val Asp Leu Asn Leu Arg Pro Thr
210         215         220
Gly Gly Gly Thr Tyr Ile Gly Arg Asn Ser Val Asp Met Cys Phe Tyr
225         230         235         240
Asp Gly Tyr Ser Thr Asn Ser Ser Ser Leu Glu Ile Arg Phe Gln Asp
245         250         255
Asp Asn Ser Lys Ser Asp Gly Lys Phe Tyr Leu Lys Lys Ile Asn Asp
260         265         270
Asp Ser Lys Glu Leu Val Tyr Thr Leu Ser Leu Leu Leu Ala Gly Lys
275         280         285
Asn Leu Thr Pro Thr Asn Gly Gln Ala Leu Asn Ile Asn Thr Ala Ser
290         295         300
Leu Glu Thr Asn Trp Asn Arg Ile Thr Ala Val Thr Met Pro Glu Ile
305         310         315         320
Ser Val Pro Val Leu Cys Trp Pro Gly Arg Leu Gln Leu Asp Ala Lys

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325					330					335					
Val	Lys	Asn	Pro	Glu	Ala	Gly	Gln	Tyr	Met	Gly	Asn	Ile	Lys	Ile	Thr
			340					345					350		
Phe	Thr	Pro	Ser	Ser	Gln	Thr	Leu	Asp	Asn	Lys	Gln	Val	Glu	Lys	Asn
		355					360					365			
Ile	Thr	Val	Thr	Ala	Ser	Val	Asp	Pro	Ala	Ile	Asp	Leu	Leu	Gln	Ala
	370					375					380				
Asp	Gly	Asn	Ala	Leu	Pro	Ser	Ala	Val	Lys	Leu	Ala	Tyr	Ser	Pro	Ala
385					390					395					400
Ser	Lys	Thr	Phe	Glu	Ser	Tyr	Arg	Val	Met	Thr	Gln	Val	His	Thr	Asn
			405						410						415
Asp	Ala	Thr	Lys	Lys	Val	Ile	Val	Lys	Leu	Ala	Asp	Thr	Pro	Gln	Leu
		420						425					430		
Thr	Asp	Val	Leu	Asn	Ser	Thr	Val	Gln	Met	Pro	Ile	Ser	Val	Ser	Trp
		435					440						445		
Gly	Gly	Gln	Val	Leu	Ser	Thr	Thr	Ala	Lys	Glu	Phe	Glu	Ala	Ala	Ala
	450					455					460				
Leu	Gly	Tyr	Ser	Ala	Ser	Gly	Val	Asn	Gly	Val	Ser	Ser	Ser	Gln	Glu
465					470					475					480
Leu	Val	Ile	Ser	Ala	Ala	Pro	Lys	Thr	Ala	Gly	Thr	Ala	Pro	Thr	Ala
				485					490						495
Gly	Asn	Tyr	Ser	Gly	Val	Val	Ser	Leu	Val	Met	Thr	Leu	Gly	Ser	Asp
		500						505					510		
Asn	Lys	Gln	Val	Glu	Lys	Asn	Ile	Thr	Val	Thr	Ala	Ser	Val	Asp	Pro
		515					520						525		
Ala	Gly	Ser	Lys	Ser	Phe	Phe	Ala	Pro	Glu	Pro	Arg	Ile	Gln	Pro	Ser
	530					535					540				
Phe	Gly	Glu	Asn	Val	Gly	Lys	Glu	Gly	Ala	Leu	Leu	Phe	Ser	Val	Asn
545					550					555					560
Leu	Thr	Val	Pro	Glu	Asn	Val	Ser	Gln	Val	Thr	Val	Tyr	Pro	Val	Tyr
				565					570						575
Asp	Glu	Asp	Tyr	Gly	Leu	Gly	Arg	Leu	Val	Asn	Thr	Ala	Asp	Ala	Ser
			580					585					590		
Gln	Ser	Ile	Ile	Tyr	Gln	Ile	Val	Asp	Glu	Lys	Gly	Lys	Lys	Met	Leu
		595					600						605		
Lys	Asp	His	Gly	Ala	Glu	Val	Thr	Pro	Asn	Gln	Gln	Ile	Thr	Phe	Lys
	610					615						620			
Ala	Leu	Asn	Tyr	Thr	Ser	Gly	Glu	Lys	Lys	Ile	Ser	Pro	Gly	Ile	Tyr
625					630					635					640
Asn	Asp	Gln	Val	Met	Val	Gly	Tyr	Tyr	Val	Asn	Asp	Asn	Lys	Gln	Gly
			645						650						655
Asn	Trp	Gln	Tyr	Lys	Ser	Leu	Asp	Val	Asn	Val	Asn	Ile	Glu	Gln	Asn
		660						665					670		
Phe	Ile	Pro	Asp	Ile	Asp	Ser	Ala	Val	Arg	Ile	Ile	Pro	Val	Asn	Tyr
		675					680						685		
Asp	Ser	Asp	Pro	Lys	Leu	Asp	Ser	Gln	Leu	Tyr	Thr	Val	Glu	Met	Thr
	690					695						700			
Ile	Pro	Ala	Gly	Val	Ser	Ala	Val	Lys	Ile	Ala	Pro	Thr	Asp	Ser	Leu
705					710					715					720
Thr	Ser	Ser	Gly	Gln	Gln	Ile	Gly	Lys	Leu	Val	Asn	Val	Asn	Asn	Pro
			725						730						735
Asp	Gln	Asn	Met	Asn	Tyr	Tyr	Ile	Arg	Lys	Asp	Ser	Gly	Ala	Gly	Asn
			740					745					750		

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Phe Met Ala Gly Gln Lys Gly Ser Phe Pro Val Lys Glu Asn Thr Ser  
 755 760 765  
 Tyr Thr Phe Ser Ala Ile Tyr Thr Gly Gly Glu Tyr Pro Asn Ser Gly  
 770 775 780  
 Tyr Ser Ser Gly Thr Tyr Ala Gly Asn Leu Thr Val Ser Phe Tyr Ser  
 785 790 795 800  
 Asn Asp Asn Lys Gln Arg Thr Glu Ile Ala Thr Lys Asn Phe Pro Val  
 805 810 815  
 Ser Thr Thr Ile Ser Leu Glu His His His His His His  
 820 825

<210> SEQ ID NO 113  
 <211> LENGTH: 2487  
 <212> TYPE: DNA  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 113

atgaataaaa ttttatttat ttttacattg tttttttctt cagggttttt tacatttgcc 60  
 gtatcggcag ataaaaatcc cggaagtga aacatgacta atactattgg tccccatgac 120  
 agggggggat cttcccccat atataatc ttaaattcct atcttacagc atacaatgga 180  
 agccatcatc tgtatgatag gatgagtttt ttatgtttgt cttctcaaaa tacctgaat 240  
 ggagcatgcc caagcagtga tgccccggc actgctacaa ttgatggcga acaaatata 300  
 acattacaat ttacggaaaa aagaagtcta attaaaagag aactgcaaat taaaggctat 360  
 aaacaatttt tgttcaaaaa tgctaattgc ccatctaac tagcacttaa ctcatctcat 420  
 tttcaatgta atagagaaca agcttcaggt gctactttat cgttatacat accagctggt 480  
 gaattaaata aattacccttt tggggggggtc tggaatgccc ttctgaagct aaatgtaaaa 540  
 agacgatatg atacaaccta tgggacttac actataaaca tcacagttaa ttaactgat 600  
 aaggaaata ttcagatgat gttaccacag ttcaaaaagta acgctcgtgt cgatcttaac 660  
 ttgcttccaa ctgggtggtg tacatatatc ggaagaaatt ctggtgatat gtgcttttat 720  
 gatggatata gtactaacag cagctcttta gagataagat ttcaggatga taattctaaa 780  
 tctgatggaa aattttatct aaagaaaata aatgatgact ccaaagaact tgtatacact 840  
 ttgtcacttc tcctggcagg taaaaattha acaccaacaa atggacaggc attaaatatt 900  
 aacctgctt ctctggaac aaactggaat agaattacag ctgtccat gccagaaatc 960  
 agtgttccgg tgtgtgtgtg gcttgacgt ttgcaattgg atgcaaaagt gaaaaatccc 1020  
 gaggtggac aatatatggg gaatattaaa attactttca caccaagtag tcaaacactc 1080  
 gacaataaac aagtagagaa aaatattact gtaacagcta gtgttgatcc tgcaattgat 1140  
 cttttgcaag ctgatggcaa tgctctgcca tcagctgtaa agttagetta ttctcccga 1200  
 tcaaaaactt ttgaaagtta cagagtaatg actcaagtcc atacaaaaga tgcaactaaa 1260  
 aaagtaattg taaacttgc tgatacacca cagcttacag atgttctgaa ttcaactggt 1320  
 caaatgccta tcagtgtgtc atggggagga caagtattat ctacaacagc caaagaattt 1380  
 gaagctgctg ctttgggata ttctgcatcc ggtgtaaatg gcgtatcatc ttctcaagag 1440  
 ttagtaatta gcgctgcacc taaaactgcc ggtaccgccc caactgcagg aaactattca 1500  
 ggagtagtat ctcttgaat gactttggga tccgacaata aacaagtaga gaaaaatatt 1560  
 actgtaacag ctagtgtcga cctgcaggg aattttatc cagatattga ttccgctggt 1620  
 cgtataatc ctgttaatta cgattcggac ccgaaactgg attcacagtt atatacgggt 1680

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gagatgacga tcctgcagg tgtaagcgca gttaaaatcg caccaacaga tagtctgaca 1740
tcttctggac agcagatcgg aaagctggtt aatgtaaaca atccagatca aaatatgaat 1800
tattatatca gaaaggattc tggcgctggt aactttatgg caggacaaaa aggatccttt 1860
cctgtcaaag agaatacgtc atacacattc tcagcaatth atactggtgg cgaataccct 1920
aatagcggat attcgtctgg tacttatgca ggaaatttga ctgtatcatt ttacagcaat 1980
gacaataaac aaagaacaga aatagcgact aaaaacttcc cagtatcaac gactatttca 2040
aaaagttttt ttgcacatga accacgaata cagccttctt ttggtgaaaa tgttgaaaag 2100
gaaggagctt tattatttag tgtgaactta actgttctctg aaaatgtatc ccaggtaacg 2160
gtctaccctg tttatgatga agattatggg ttaggacgac tagtaaaatac cgctgatgct 2220
tcccaatcaa taatctacca gattgttgat gagaaggga aaaaaatggt aaaagatcat 2280
ggtgcagagg ttacacctaa tcaacaata acttttaaag cgctgaatta tactagcggg 2340
gaaaaaaaaa tatctctcgg aatatataac gatcaggtta tggttggta ctacgtaaac 2400
gacaataaac aaaccgagat tgcaccaag aatthtccgg tgagcaccac catcagcctc 2460
ctcgagcacc accaccacca cactga 2487

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&lt;210&gt; SEQ ID NO 114

&lt;211&gt; LENGTH: 828

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Escherichia coli

&lt;400&gt; SEQUENCE: 114

```

Met Asn Lys Ile Leu Phe Ile Phe Thr Leu Phe Phe Ser Ser Gly Phe
 1             5             10             15
Phe Thr Phe Ala Val Ser Ala Asp Lys Asn Pro Gly Ser Glu Asn Met
 20             25             30
Thr Asn Thr Ile Gly Pro His Asp Arg Gly Gly Ser Ser Pro Ile Tyr
 35             40             45
Asn Ile Leu Asn Ser Tyr Leu Thr Ala Tyr Asn Gly Ser His His Leu
 50             55             60
Tyr Asp Arg Met Ser Phe Leu Cys Leu Ser Ser Gln Asn Thr Leu Asn
 65             70             75             80
Gly Ala Cys Pro Ser Ser Asp Ala Pro Gly Thr Ala Thr Ile Asp Gly
 85             90             95
Glu Thr Asn Ile Thr Leu Gln Phe Thr Glu Lys Arg Ser Leu Ile Lys
100            105            110
Arg Glu Leu Gln Ile Lys Gly Tyr Lys Gln Phe Leu Phe Lys Asn Ala
115            120            125
Asn Cys Pro Ser Lys Leu Ala Leu Asn Ser Ser His Phe Gln Cys Asn
130            135            140
Arg Glu Gln Ala Ser Gly Ala Thr Leu Ser Leu Tyr Ile Pro Ala Gly
145            150            155            160
Glu Leu Asn Lys Leu Pro Phe Gly Gly Val Trp Asn Ala Val Leu Lys
165            170            175
Leu Asn Val Lys Arg Arg Tyr Asp Thr Thr Tyr Gly Thr Tyr Thr Ile
180            185            190
Asn Ile Thr Val Asn Leu Thr Asp Lys Gly Asn Ile Gln Ile Trp Leu
195            200            205
Pro Gln Phe Lys Ser Asn Ala Arg Val Asp Leu Asn Leu Arg Pro Thr
210            215            220

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Gly Gly Gly Thr Tyr Ile Gly Arg Asn Ser Val Asp Met Cys Phe Tyr  
 225 230 235 240  
 Asp Gly Tyr Ser Thr Asn Ser Ser Ser Leu Glu Ile Arg Phe Gln Asp  
 245 250 255  
 Asp Asn Ser Lys Ser Asp Gly Lys Phe Tyr Leu Lys Lys Ile Asn Asp  
 260 265 270  
 Asp Ser Lys Glu Leu Val Tyr Thr Leu Ser Leu Leu Leu Ala Gly Lys  
 275 280 285  
 Asn Leu Thr Pro Thr Asn Gly Gln Ala Leu Asn Ile Asn Thr Ala Ser  
 290 295 300  
 Leu Glu Thr Asn Trp Asn Arg Ile Thr Ala Val Thr Met Pro Glu Ile  
 305 310 315 320  
 Ser Val Pro Val Leu Cys Trp Pro Gly Arg Leu Gln Leu Asp Ala Lys  
 325 330 335  
 Val Lys Asn Pro Glu Ala Gly Gln Tyr Met Gly Asn Ile Lys Ile Thr  
 340 345 350  
 Phe Thr Pro Ser Ser Gln Thr Leu Asp Asn Lys Gln Val Glu Lys Asn  
 355 360 365  
 Ile Thr Val Thr Ala Ser Val Asp Pro Ala Ile Asp Leu Leu Gln Ala  
 370 375 380  
 Asp Gly Asn Ala Leu Pro Ser Ala Val Lys Leu Ala Tyr Ser Pro Ala  
 385 390 395 400  
 Ser Lys Thr Phe Glu Ser Tyr Arg Val Met Thr Gln Val His Thr Asn  
 405 410 415  
 Asp Ala Thr Lys Lys Val Ile Val Lys Leu Ala Asp Thr Pro Gln Leu  
 420 425 430  
 Thr Asp Val Leu Asn Ser Thr Val Gln Met Pro Ile Ser Val Ser Trp  
 435 440 445  
 Gly Gly Gln Val Leu Ser Thr Thr Ala Lys Glu Phe Glu Ala Ala Ala  
 450 455 460  
 Leu Gly Tyr Ser Ala Ser Gly Val Asn Gly Val Ser Ser Ser Gln Glu  
 465 470 475 480  
 Leu Val Ile Ser Ala Ala Pro Lys Thr Ala Gly Thr Ala Pro Thr Ala  
 485 490 495  
 Gly Asn Tyr Ser Gly Val Val Ser Leu Val Met Thr Leu Gly Ser Asp  
 500 505 510  
 Asn Lys Gln Val Glu Lys Asn Ile Thr Val Thr Ala Ser Val Asp Pro  
 515 520 525  
 Ala Gly Asn Phe Ile Pro Asp Ile Asp Ser Ala Val Arg Ile Ile Pro  
 530 535 540  
 Val Asn Tyr Asp Ser Asp Pro Lys Leu Asp Ser Gln Leu Tyr Thr Val  
 545 550 555 560  
 Glu Met Thr Ile Pro Ala Gly Val Ser Ala Val Lys Ile Ala Pro Thr  
 565 570 575  
 Asp Ser Leu Thr Ser Ser Gly Gln Gln Ile Gly Lys Leu Val Asn Val  
 580 585 590  
 Asn Asn Pro Asp Gln Asn Met Asn Tyr Tyr Ile Arg Lys Asp Ser Gly  
 595 600 605  
 Ala Gly Asn Phe Met Ala Gly Gln Lys Gly Ser Phe Pro Val Lys Glu  
 610 615 620  
 Asn Thr Ser Tyr Thr Phe Ser Ala Ile Tyr Thr Gly Gly Glu Tyr Pro  
 625 630 635 640  
 Asn Ser Gly Tyr Ser Ser Gly Thr Tyr Ala Gly Asn Leu Thr Val Ser

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645				650				655							
Phe	Tyr	Ser	Asn	Asp	Asn	Lys	Gln	Arg	Thr	Glu	Ile	Ala	Thr	Lys	Asn
			660												670
Phe	Pro	Val	Ser	Thr	Thr	Ile	Ser	Lys	Ser	Phe	Phe	Ala	Pro	Glu	Pro
			675												685
Arg	Ile	Gln	Pro	Ser	Phe	Gly	Glu	Asn	Val	Gly	Lys	Glu	Gly	Ala	Leu
			690												700
Leu	Phe	Ser	Val	Asn	Leu	Thr	Val	Pro	Glu	Asn	Val	Ser	Gln	Val	Thr
			705												720
Val	Tyr	Pro	Val	Tyr	Asp	Glu	Asp	Tyr	Gly	Leu	Gly	Arg	Leu	Val	Asn
			725												735
Thr	Ala	Asp	Ala	Ser	Gln	Ser	Ile	Ile	Tyr	Gln	Ile	Val	Asp	Glu	Lys
			740												750
Gly	Lys	Lys	Met	Leu	Lys	Asp	His	Gly	Ala	Glu	Val	Thr	Pro	Asn	Gln
			755												765
Gln	Ile	Thr	Phe	Lys	Ala	Leu	Asn	Tyr	Thr	Ser	Gly	Glu	Lys	Lys	Ile
			770												780
Ser	Pro	Gly	Ile	Tyr	Asn	Asp	Gln	Val	Met	Val	Gly	Tyr	Tyr	Val	Asn
			785												800
Asp	Asn	Lys	Gln	Gly	Asn	Trp	Gln	Tyr	Lys	Ser	Leu	Asp	Val	Asn	Val
			805												815
Asn	Ile	Glu	Gln	Leu	Glu	His	His	His	His	His	His				
			820												825

<210> SEQ ID NO 115  
 <211> LENGTH: 1014  
 <212> TYPE: DNA  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 115

```

gcagataaaa atccccgaag tgaaaacatg actaataacta ttggtcccca tgacaggggg      60
ggatcttccc ccatatataa tatcttaaat tcctatctta cagcatacaa tggaagccat      120
catctgtatg ataggatgag ttttttatgt ttgtcttctc aaaatacact gaatggagca      180
tgcccaagca gtgatgcccc tggcactgct acaattgatg gcgaacacaaa tataacatta      240
caatttacgg aaaaaagaag tctaattaa agagaactgc aaattaaagg ctataaacia      300
tttttgttca aaaatgctaa ttgcccatct aaactagcac ttaactcadc tcattttcaa      360
tgtaaatagag aacaagcttc aggtgctact ttatcgttat acataaccagc tggatgaatta      420
aataaattac cttttggggg ggtctggaat gccgttctga agctaaatgt aaaaagacga      480
tatgatacaa cctatgggac ttacactata aacatcacag ttaatttaac tgataagggg      540
aatattcaga tatggttacc acagttcaaa agtaacgctc gtgtcgatct taacttgctg      600
ccaactggtg gtggtacata tatcggaaga aattctgttg atatgtgctt ttatgatgga      660
tatagtacta acagcagctc tttagagata agatttcagg atgataattc taaatctgat      720
ggaaaatttt atctaaagaa aataaatgat gactccaaag aacttgata cactttgtca      780
cttctcctgg caggtaaaaa ttaaacacca acaaatggac aggcattaaa tattaacact      840
gcttctctgg aaacaaactg gaatagaatt acagctgtca ccatgccaga aatcagtgtt      900
ccggtgttgt gttggcctgg acgtttgcaa ttggatgcaa aagtgaaaaa tcccagggct      960
ggacaatata tggggaatat taaaattact ttcacaccaa gtagtcaaac actc      1014
    
```

<210> SEQ ID NO 116

-continued

&lt;211&gt; LENGTH: 441

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Escherichia coli

&lt;400&gt; SEQUENCE: 116

```

gtagagaaaa atattactgt aacagctagt gttgatcctg caattgatct tttgcaagct    60
gatggcaatg ctctgccatc agctgtaaag ttagcttatt ctcccgcatc aaaaactttt    120
gaaagttaca gagtaatgac tcaagttcat acaaacgatg caactaaaaa agtaattggt    180
aaacttgctg atacaccaca gcttacagat gttctgaatt caactgttca aatgcctatc    240
agtgtgtcat ggggaggaca agtattatct acaacagcca aagaatttga agctgctgct    300
ttgggatatt ctgcatcggg tgtaaatggc gtatcatctt ctcaagagtt agtaattagc    360
gctgcaccta aaactgccgg taccgcccc aactgcaggaa actattcagg agtagtatct    420
cttgtaatga ctttgggatc c                                         441

```

&lt;210&gt; SEQ ID NO 117

&lt;211&gt; LENGTH: 1020

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Escherichia coli

&lt;400&gt; SEQUENCE: 117

```

gcagataaaa ttcccgagaga tgaagcata actaatatct tggcccggcg tgacaggaac    60
gaatcttccc ccaaacataa tatattaaat aaccatatta cagcatacag tgaagtcatt    120
actctgtatg ataggatgac ttttttatgt ttgtcttctc acaatacact taatggagca    180
tgtccaacca gtgagaatcc tagcagttca tcggtcagcg gtgaaacaaa tataacatta    240
caatttacgg aaaaaagaag ttttaataaaa agagagctac aaattaaagg ctataaacia    300
ttattgttca aaagtgttaa ctgcccattc ggcctaacac ttaactcagc tcattttaac    360
tgtaataaaa acgcggtctc aggtgcaagt ttatatttat atattcctgc tggcgaacta    420
aaaaatttgc cttttgttgg tatctgtggat gctactctga agttaagagt aaaaagacga    480
tatagtgaga cctatggaac ttacactata aatatcacta ttaaatatc tgataagggaa    540
aatattcaga tatggttacc tcagttcaaa agtgacgctc gcgtcgatct taacttgcgt    600
ccaactggtg ggggcacata tattggaaga aattctgttg atatgtgctt ttatgatgga    660
tatagtacta acagcagctc tttggagata agatttcagg ataacaatcc taaatctgat    720
gggaaatctt atctaaggaa aataaatgat gacaccaaag aaattgcata tactttgtca    780
cttctcttgg cgggtaaaag ttttaactcca acaaatggaa cgtcattaaa tattgctgac    840
gcagcttctc tggaaacaaa ctggaataga attacagctg tcaccatgcc agaaatcagt    900
gttccggtgt tgtgttggcc tggacgtttg caattggatg caaaagtgga aaatcccgag    960
gctggacaat atatgggtaa tattaatggt actttcacac caagtagtca aacactctag    1020

```

&lt;210&gt; SEQ ID NO 118

&lt;211&gt; LENGTH: 435

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Escherichia coli

&lt;400&gt; SEQUENCE: 118

```

gtagagaaaa atatcactgt aacagctagt gttgatccta caattgatat tttgcaagct    60
gatggtagta gtttacctac tgctgtagaa ttaacctatt cacctgcggc aagtcgtttt    120
gaaaattata aaatcgcaac taaagttcat acaaatgtta taaataaaaa tgtactagtt    180
aagcttgtaa atgatccaaa acttacaaat gttttggatt ctacaaaaca actccccatt    240

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actgtatcat atggaggaaa gactctatca accgcagatg tgacttttga acctgcagaa 300
ttaaattttg gaacgtcagg tgtaactggt gtatcttctt cccaagattt agtgattggt 360
gcgactacag cacaagcacc aacggcgagg aattatagtg gggtcgttcc tatcttaatg 420
accttagcat cataa 435

```

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<210> SEQ ID NO 119
<211> LENGTH: 1020
<212> TYPE: DNA
<213> ORGANISM: Escherichia coli

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```

<400> SEQUENCE: 119

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```

gcagataaaa ttcccggaga tgagaatata actaatattt ttggcccgcg tgacaggaac 60
gaatcttccc ccaaacataa tatattaaat gactatatta cagcatacag tgaaagtcat 120
actctgtatg ataggatgat ttttttatgt ttgtcttctc aaaatacact taatggagca 180
tgtccaacca gtgagaatcc tagcagttca tcggtcagtg gcgaacaaa tataacatta 240
caatttacgg aaaaaagaag ttaattaaa agagagctac aaattaaagg ctataaacga 300
ttattgttca aagggtgctaa ctgccatcc tacctaacac ttaactcagc tcattatacc 360
tgcaatagaa actcggcttc aggtgcaagt ttatatttat atattcctgc tggcgaacta 420
aaaaatttac cttttggtgg tatctgggat gctactctga agttaagagt aaaaagacga 480
tatgatcaga cctatggaac ttacactata aatatactg ttaaattaac tgataagga 540
aatattcaga tatggttacc tcagttcaaa agtgacgctc gcgtogactc taacttgcgt 600
ccaactggtg ggggcacata tattggaaga aattctgttg atatgtgctt ttatgatgga 660
tatagtacta acagcagctc tttggagcta agatttcagg ataacaatcc taaatctgat 720
gggaaatttt atctaaggaa aataaatgat gacaccaaag aaattgcata tactttgtca 780
cttctcttgg cgggtaaaag ttaactcca acaaatggaa cgtcattaaa tattgctgac 840
gcagcttctc tggaaataaa ctggaataga attacagctg tcaccatgcc agaaatcagt 900
gttcgggtgt tgtgttgcc tggacgtttg caattggatg caaaagtgga aaatcccag 960
gccggacaat atatgggtaa tattaatatt actttcacac caagtagtca aacactctag 1020

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<210> SEQ ID NO 120
<211> LENGTH: 459
<212> TYPE: DNA
<213> ORGANISM: Escherichia coli

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<400> SEQUENCE: 120

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```

gtagagaaaa atattactgt gacagccagt gttgatccta ctattgatat tcttcaagca 60
aatggttctg cgctaccgac agctgtagat ttaacttacc tacctggtgc aaaaactttt 120
gaaaattaca gtgttctaac ccagatttac acaaatgacc cttcaaaagg ttagatggt 180
cgactggttg atacaccgaa acttacaaat attttgcaac cgacatctac cattcctctt 240
actgtctcat gggcagggaa gacattaagt acaagtgctc agaagattgc agttggcgat 300
ctgggttttg gttccaccgg aacggcaggt gtttcgaata gtaaagaatt agtaattgga 360
gcaactacat ccggaactgc accaagtgca ggtaagtatc aaggcgtcgt ttccattgta 420
atgactcaat cgacagacac agccgcgcct gttccttaa 459

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<210> SEQ ID NO 121
<211> LENGTH: 441
<212> TYPE: DNA

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<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 121

gtagagaaaa atattactgt gacagccagt gttgaccta ctattgatat ttttcaagca	60
aatggttctg cgctaccgac agctgtagat ttaacttacc tacctggtgc aaaaactttt	120
gaaaattaca gtgttctaac ccagatttac acaaatgacc cttcaaaagg tttagatggt	180
cgactggttg atacaccgaa acttacaaat attttgcaac cgacatctac cattcctctt	240
actgtctcat gggcagggag gacattaagt acaagtgtc agaagatgc agttggcgat	300
ctgggttttg gttccaccgg aacggcaggt gtttcgaata gtaaagaatt agtaattgga	360
gcaactacat cggaaactgc accaagtgc ggtaagtacc aaggcgtcgt ttcattgta	420
atgactcaat cgacaaacta a	441

<210> SEQ ID NO 122

<211> LENGTH: 1038

<212> TYPE: DNA

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 122

gggcgatacc cggaaactac agtaggtaat ctgacgaaga gttttcaagc cctcgtctg	60
gatagaagcg tacaatcacc aatataaac atctttacga atcatgtggc tggatatagt	120
ttgagtcata gcttatatga caggattggt tttttatgta catcctcgtc gaatccgggt	180
aatggtgctt gcccaacct tggaaacct ggagttcaat acggtaact aaccataacc	240
ttgcagttta cagaaaaaag aagtctgata aaaagaaata ttaatcttgc aggtaataag	300
aaaccaatat gggagaatca gagttgagc tttagcaatc taatggtgtt gaattcgaag	360
tcttgagct gtggggtta cggaaatgct aacggaacac ttctaaatct gtatatccct	420
gcaggagaaa tcaacaaatt gccttttga gggataggg aggcaactct gatcttacgc	480
ttatcaagat atggcgaagt cagtagcacc cattacggca attataccgt aaatattacg	540
gttgatttaa ctgataaagg taatattcag gtatggcttc cagggtttca cagcaacccg	600
cgtgtagacc tgaatctgag ccctatcggg aattataaat atagtggtag taattcactc	660
gacatgtggt tctatgatgg atatagtaca aacagtgata gcatggtaat aaagttccag	720
gatgataatc ctaccaatc atctgaatat aatctttata agataggggg cactgaaaaa	780
ttaccatatg ctgtttcact gcttatggga gaaaaaatat tttatccagt gaatggtcaa	840
tcatttacta tcaatgacag tagtgactc gaaacaaact ggaatcgagt aaccgcagtt	900
gctatgccgg aagttaatgt tccagtatta tgctggccag caagattgct attaaatgct	960
gatgtaaatg ctcccgatgc aggacagtat tcaggacaga tatatataac atttacacc	1020
agtgtcgaaa atttatga	1038

<210> SEQ ID NO 123

<211> LENGTH: 447

<212> TYPE: DNA

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 123

gtcgagaaga ccattagcgt tacggcgagt gttgaccca ctggtgacct tctgcaatct	60
gatggctctg cgctgccgaa ctctgtcgca ttaacctatt ctccggtgt aaataatgtt	120
gaagctcaca ccatcaacac cgtgttcat acaaatgact cagataaagg tgtgtgtgtg	180
aagctgtcag cagatccagt cctgtccaat gttctgaatc caaccctgca aattcctggt	240

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tctgtgaatt tgcagggaaa accactgagc acaacaggca ttaccatoga ctccaatgat	300
ctgaactttg cttcgagtgg tgtaataaaa gtttcttcta cgcagaaaact ttcaatccat	360
gcagatgcta ctccgggtaac tggcggcgca ctaacagctg gtcaatatca gggactcgta	420
tcaattatoc tgactaagtc aacgtaa	447

<210> SEQ ID NO 124  
 <211> LENGTH: 1038  
 <212> TYPE: DNA  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 124

ggggataacc cggaaactac agtaggtaat ctgacgaaga gttttcaagc ccctcgtctg	60
gatagaagcg tacaatcacc aatatataac atctttacga atcatgtggc tggatatagt	120
ttgagtcata gattatatga caggattgtt tttgtatgta catcctcgtc gaatccgggt	180
aatggtgctt gcccaacatc tggaacatct agagttgaat acggtaactac aaccataacc	240
ttgcagttta cagaaaaaag aagtctgata aaaagaaata ttaatcttgc aggtaataag	300
aaaccaatat gggagaatca gagttcgac actagcaatc taatggtggt gaattcgaag	360
tcttggctct gtggggctct aggaaatgct aacggaacac ttctaaatct gtatatccct	420
gcagagagaaa tcaacaaatt gccttttggg gggatatggg aggcaactct gatcttacgc	480
ttatcaagat atggcgaagt cagtagcacc cattaacgca attataccgt aaatattacg	540
gttgatttaa ctgataaagg taatattcag gtatggcttc cagggtttca cagcaaccgc	600
cgtgtagacc tgaatctgca cccatcgggt aattataaat atagtggtag taattcactc	660
gacatgtggt tctatgatgg atatagtaca aacagtgata gcatggtaat aaagttccag	720
gatgataatc ctaccaatc atctgaatat aatctttata agataggggg cactgaaaaa	780
ttaccatag ctgtttcact gcttatggga gaaaaaatat tttatccagt gaatggtcaa	840
tcatttacta tcaatgacag tagtgtactc gaaacaaact ggaatcgagt aaccgcagtt	900
gctatgccgg aagttaatgt tccagtatta tgctggccag caagattgct attaaatgct	960
gatgtaaag ctcccgatgc aggacagtat tcaggacaga tatatataac atttacacce	1020
agtgtcgaaa atttatga	1038

<210> SEQ ID NO 125  
 <211> LENGTH: 432  
 <212> TYPE: DNA  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 125

gtcgaaaaaa atattactgt gagggcaagt gttgacccta aacttgatct tctgcaagca	60
gatggaactt cactgccgga ctctatcgca ttaacctatt ctteggcttc aaataatttt	120
gaagtttact ctcttaatac tgctattcat acaaatgaca aaaccaaggc agttgtagt	180
aagctgtcag ctccagcagt tctgtccaat attatgaagc caagctcgca aattccgatg	240
aaagtgactt tgggggggaa gacgctgagt acagctgatg ctgagtttgc tgctgatact	300
ctgaactttg gtgcatctgg tgttgaaaac gtttcttccg ttcaacagct tacgattcat	360
gcagaagctg ctccgcctga ggcaggtaat taccaaggtg ttatttctct tatcatgact	420
caaaaaactt aa	432

<210> SEQ ID NO 126

-continued

&lt;211&gt; LENGTH: 444

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Escherichia coli

&lt;400&gt; SEQUENCE: 126

```

gtcgagaaga ccattagcgt tacggcgagt gttgaccga ctgttgacct tctgcaatct    60
gatggctctg cgctgccgaa ctctgtcgca ttaacctatt ctccggctgt aggggggttt    120
gaagctcaca ccatacaac cggtgttcat acaaatgacc cagctaaagg tgttattgtg    180
aagctgtcag cagaaccagt cctgtccaat gtactgaatc caacctgca aattcctgtt    240
tctgtgaatt tcgaggaaa aaaactgacc acaacaggca ctaccatcga atccaataaa    300
ctgaactttg cttcgagtgg tgttgataaa gttttctcta cgcagaaact ttcaatccat    360
gcagatacta ctcaggtaac tggcggacta acagctggtc aatatcaggg gctcgtatca    420
attatcctga ctcagtcaac gtaa                                           444

```

&lt;210&gt; SEQ ID NO 127

&lt;211&gt; LENGTH: 1038

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Escherichia coli

&lt;400&gt; SEQUENCE: 127

```

gggcgatacc cggaaactac agtaggtaat ctgacgaaga gttttcaagc ccctcgtcag    60
gatagaagcg tacaatcacc aatatataac atctttacga atcatgtggc tggatatagt    120
ttgagtcata acttatatga caggattgtt tttttatgta catcctcgtc gaatccggtt    180
aatggtgctt gcccaacctt tgaacatct ggagttcaat acggtactac aaccataacc    240
ttgcagttta cagaaaaaag aagtctgata aaaagaaata ttaatcttgc aggtaataag    300
aaaccaatat gggagaatca gagttgcgac actagcaatc taatgggtgt gaattcgaag    360
tcttggctct gtggggctta cggaaatgct aacggaacac ttctaaatct gtatatccct    420
gcaggagaaa tcaacaaatt gccttttggg gggatatggg aggcaactct gatcttacgc    480
ttatcaagat atggcgaagt cagtagcacc cattacggca attataccgt aaatattacg    540
gttgatttaa ctgataaagg taatattcag gtatggcttc cagggtttca cagcaaccgg    600
cgtgtagacc tgaatctgca ccctatcggg aattataaat atagtggtag taattcactc    660
gacatgtggt tctatgatgg atatagtaca aacagtgata gcatggtaat aaagttccag    720
gatgataatc ctacctatc atctgaatat aatctttata agataggggg cactgaaaaa    780
ttaccataty ctgtttcact gcttatggga gaaaaaatat tttatccagt gaatgggtcaa    840
tcatttacta tcaatgacag tagtgactc gaaacaaact ggaatcgagt aaccgcagtt    900
gctatgccgg aagttaatgt tccagtatta tgctggccag caagattgct attaaatgct    960
gatgtaaatg ctcccgatgc aggacagtat tcaggacaga tatatataac atttacacc    1020
agtgtcgaaa atttatga                                           1038

```

&lt;210&gt; SEQ ID NO 128

&lt;211&gt; LENGTH: 438

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Escherichia coli

&lt;400&gt; SEQUENCE: 128

```

gtcgaaaaaa atattactgt gagggcaagt gttgacccta aacttgatct tctgcaagca    60
gatggaactt cactgccgga ctctatcgca ttaacctatt ctccggcttc aaataathtt    120
gaagtttact ctcttaatac tgctattcat acaaatgaca aaagcaaggg agttgtagtg    180

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aagctgtcag cttcaccagt tctgtccaat attatgaagc caaactcgca aattccgatg	240
aaagtgactt tgggggggaa gacgctgaat acaactgata ctgagtttac tgttgatact	300
ctgaactttg gtacatctgg tgttgaaaac gtttcttcca ctcaacagct tacgattcat	360
gcagacacac aaggaactgc gctgaggca ggcaattacc aaggtattat ttctcttatc	420
atgactcaaa aaacttaa	438

<210> SEQ ID NO 129  
 <211> LENGTH: 1041  
 <212> TYPE: DNA  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 129

caatcatggc atacgaaagt agaggctggt tcaataaata aaacagagtc gataggcccc	60
atagaccgaa gtgctgtctg atcgtatcct gctcattata tatttcatga acatggtgct	120
ggttacaata aagatcactc tctttttgac aggatgacgt ttttatgtat gtcacaca	180
gatgcatcta aaggtgcatg tccgacagga gaaaactcca aatcctctca aggggagact	240
aatattaagc taatatttac tgaagagaaa agtctggcca gaaaaacatt aaacttaaaa	300
ggatataaga gatttttata tgaatcagat agatgcattc attatgtcga taaaatgaat	360
ctcaattctc atactgttaa atgtgtagggt tcattcacia gaggagtaga ttctacttta	420
tatatccac aaggtgaaat tgatgggctt ctaactggag gtatatggga ggcaacacta	480
gagttacgag tcaaaaggca ttacgactat aatcatggta cttacaaagt taatcacaca	540
gttgatttga cagacaaagg aaatattcag gtctggacac caaagtttca tagcgatcct	600
agaattgatc tgaatttacg tcttgaaggt aatggtaaat attctggtag taacgtgctt	660
gagatgtgtc tctatgatgg ctatagtaca catagtcaaa gtatagaaat gaggtttcag	720
gatgactcac aaacaggaaa taatgaatat aatcttataa aaactggaga gccattaaaa	780
aaattgcoat ataaactttc tcttctttta ggaggacgag agttttatcc aaataatgga	840
gaggctttta ctattaatga tactctgca ttgtttataa actggaatcg tattaagtct	900
gtatccttac cacagattag tattccagta ctatgctggc cagcaaactt gacatttatg	960
tcagagctaa ataatccaga agcgggtgag tattcaggaa tacttaacgt aacatttact	1020
cctagtagtt caagtctgta a	1041

<210> SEQ ID NO 130  
 <211> LENGTH: 444  
 <212> TYPE: DNA  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 130

gccgagaaaa atatcactgt aactgctagc gttgatccaa ctatcgatct gatgcaatct	60
gatggcacag cgttaccaag tgcagttaat attgcatac ttccaggaga gaaaagattt	120
gaatctgctc gtatcaatac ccaagttcat accaataata aaactaaggg tattcagata	180
aagcttacta atgataatgt ggtaatgact aacttatctg atccaagcaa gactattcct	240
ttagaggttt cattcgctgg cactaagctg agcacagctg caacatctat tactgccgat	300
caattaaatt ttggcgcagc tgggttagag acagtttctg caactaagga actcgttatt	360
aatgcaggaa gcaccagca aactaatatt gtagctggta actatcaagg attggtgtca	420
attgtgctta ctcaagaacc ttaa	444

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<210> SEQ ID NO 131
<211> LENGTH: 441
<212> TYPE: DNA
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 131
gcagcggggc ccactctaac caaagaactg gcattaaatg tgctttctcc tgcagctctg    60
gatgcaactt gggctcctca ggataattta acattatcca atactggcgt ttetaaact    120
ttggtgggtg ttttgactct ttcaaatacc agtattgata cagttagcat tgcgagtaca    180
aatgtttctg atacatctaa gaatggtaca gtaacttttg cacatgagac aaataactct    240
gctagccttg ccaccacat ttcaacagat aatgccaca ttacggttga taaaaatget    300
ggaaatacga ttgttaaac tacaaatggg agtcagttgc caactaattt accacttaag    360
tttattacca ctgaaggtaa cgaacattta gtttcaggta attaccgtgc aaatataaca    420
attacttcga caattaata a                                441

```

```

<210> SEQ ID NO 132
<211> LENGTH: 432
<212> TYPE: DNA
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 132
gcagtgggcc caacgaaaga tatgagtta ggtgcaaatt taacttcaga gcctacatta    60
gctattgatt ttacgcctat tgaaaatatt tatgtaggtg ccaattatgg taaagatatt    120
ggaacccttg tttcacaaac aaatgattta acagatatta cattgatgtc atctcgcagc    180
gttgttgatg gtcgccagac tggttttttt accttcattg actcatcagc cacttacaaa    240
attagtacaa aactgggatc atcgaatgat gtaaacattc aagaaattac tcaaggagct    300
aaaattactc ctgttagtgg agagaaaact ttgcctaaaa aattcactct taagctacat    360
gcacacagga gtagcagtac agttccaggt acgtatactg ttggtcttaa cgtaaccagt    420
aatgttatTT aa                                432

```

```

<210> SEQ ID NO 133
<211> LENGTH: 1038
<212> TYPE: DNA
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 133
gggcgatacc cggaaactac agtaggtaat ctgacgaaga gttttcaagc ccctcgtctg    60
gatagaagcg tacaatcacc aatatataac atctttacga atcatgtggc tggatatagt    120
ttgagtcata gattatatga caggattggt tttgtatgta catcctcgtc gaatccggtt    180
aatggtgctt gcccaacat tggaaacatct ggagttgaat acggtactac aaccataacc    240
ttgcagttta cagaaaaaag aagtctgata aaaagaaata ttaatcttgc aggtaataag    300
aaaccaatat gggagaatca gagttgcgac ttagcaatc taatggtggt gaattcgaag    360
tcttggctct gtggggctca aggaaatgct aacggaacac ttctaaatct gtatatccct    420
gcaggagaaa tcaacaaatt gccttttggg gggatattgg aggcaactct gatcttacgc    480
ttatcaagat atggcgaagt cagtagcacc cattacggca attatacgt aaatattacg    540
gttgatttaa ctgataaagg taatattcag gtatggcttc cagggttca cagcaaccgg    600
cgtgtagacc tgaatctgca ccctatcggg aattataaat atagtggtag taattcactc    660
gacatgtggt tctatgatgg atatagtaca aacagtgata gcatggtaat aaagtccag    720

```

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```

gatgataatc ctaccaatc atctgaatat aatctttata agagaggggg cactgaaaa 780
ttaccatatg ctgtttcact gcttatggga ggaaaaatat tttatccagt gaatggtcaa 840
tcatttacta tcaatgacag tagtgtactc gaaacaaact ggaatcgagt aaccgcagtt 900
gctatgccgg aagttaatgt tccagtatta tgctggccag caagattgct attaaatgct 960
gatgtaaatg ctcccgatgc aggacagtat tcaggacaga tatatataac atttacaccc 1020
agtgtcgaaa atttatga 1038

```

```

<210> SEQ ID NO 134
<211> LENGTH: 465
<212> TYPE: DNA
<213> ORGANISM: Escherichia coli

```

```

<400> SEQUENCE: 134

```

```

atgaagaaaa caattggttt aattctaatt cttgcttcat tcggcagcca tgccagaaca 60
gaaatagcga ctaaaaaact cccagtatca acgactattt caaaaagtgt ttttgccct 120
gaaccacaaa tccagccttc ttttgtaaa aatgttgaa aggaaggaga tttattattt 180
agtgtgagct taattgttcc tgaaaatgta tcccaggtaa cggctaccc tgtttatgat 240
gaagattatg gattaggacg actcgtaaat accgctgatg attccaatc aataatctac 300
cagattgttg atgataaagg gaaaaaatg ttaaagatc atggtacaga ggttacgcct 360
aatcaacaaa taacttttaa agcgtgaat tatactagcg gagataaaga aatacctcct 420
gggatataata acgatcaggt tatggttggt tactatgtaa actaa 465

```

```

<210> SEQ ID NO 135
<211> LENGTH: 154
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

```

```

<400> SEQUENCE: 135

```

```

Met Lys Lys Thr Ile Gly Leu Ile Leu Ile Leu Ala Ser Phe Gly Ser
1           5           10          15
His Ala Arg Thr Glu Ile Ala Thr Lys Asn Phe Pro Val Ser Thr Thr
                20           25           30
Ile Ser Lys Ser Phe Phe Ala Pro Glu Pro Gln Ile Gln Pro Ser Phe
            35           40           45
Gly Lys Asn Val Gly Lys Glu Gly Asp Leu Leu Phe Ser Val Ser Leu
50           55
Ile Val Pro Glu Asn Val Ser Gln Val Thr Val Tyr Pro Val Tyr Asp
65           70           75           80
Glu Asp Tyr Gly Leu Gly Arg Leu Val Asn Thr Ala Asp Asp Ser Gln
            85           90           95
Ser Ile Ile Tyr Gln Ile Val Asp Asp Lys Gly Lys Lys Met Leu Lys
100          105          110
Asp His Gly Thr Glu Val Thr Pro Asn Gln Gln Ile Thr Phe Lys Ala
115          120          125
Leu Asn Tyr Thr Ser Gly Asp Lys Glu Ile Pro Pro Gly Ile Tyr Asn
130          135          140
Asp Gln Val Met Val Gly Tyr Tyr Val Asn
145          150

```

```

<210> SEQ ID NO 136
<211> LENGTH: 504
<212> TYPE: DNA

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-continued

&lt;213&gt; ORGANISM: Escherichia coli

&lt;400&gt; SEQUENCE: 136

```

atggtgaaaa aaattattcc ggctattgca ttaattgcag gaacttcgg agtggtaaat    60
gcaggaaact ggcaatataa atctctggat gtaaagttaa atattgagca aaattttatt    120
ccagatattg attccgctgt tcgtataata cctgttaatt acgattcggga tccgaaactg    180
aattcacagt tatatacggg tgagatgacg atccctgcag gtgtaagcgc agttaaatac    240
gtaccaacag atagtctgac atcttctgga cagcagatcg gaaagctggt taatgtaaac    300
aatccagatc aaaatatgaa ttattatatac agaaaggatt ctggcgctgg taagtttatg    360
gcagggcaaa aaggatcctt ttctgtcaaa gagaatacgt catacacatt ctcagcaatt    420
tatactggtg gcgaataccc taatagcgga tattcgtctg gtacttatgc aggacatttg    480
actgtatcat tttacagcaa ttaa                                           504

```

&lt;210&gt; SEQ ID NO 137

&lt;211&gt; LENGTH: 167

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Escherichia coli

&lt;400&gt; SEQUENCE: 137

```

Met Leu Lys Lys Ile Ile Pro Ala Ile Ala Leu Ile Ala Gly Thr Ser
 1                               5 10 15
Gly Val Val Asn Ala Gly Asn Trp Gln Tyr Lys Ser Leu Asp Val Asn
 20 25 30
Val Asn Ile Glu Gln Asn Phe Ile Pro Asp Ile Asp Ser Ala Val Arg
 35 40 45
Ile Ile Pro Val Asn Tyr Asp Ser Asp Pro Lys Leu Asn Ser Gln Leu
 50 55 60
Tyr Thr Val Glu Met Thr Ile Pro Ala Gly Val Ser Ala Val Lys Ile
 65 70 75 80
Val Pro Thr Asp Ser Leu Thr Ser Ser Gly Gln Gln Ile Gly Lys Leu
 85 90 95
Val Asn Val Asn Asn Pro Asp Gln Asn Met Asn Tyr Tyr Ile Arg Lys
 100 105 110
Asp Ser Gly Ala Gly Lys Phe Met Ala Gly Gln Lys Gly Ser Phe Ser
 115 120 125
Val Lys Glu Asn Thr Ser Tyr Thr Phe Ser Ala Ile Tyr Thr Gly Gly
 130 135 140
Glu Tyr Pro Asn Ser Gly Tyr Ser Ser Gly Thr Tyr Ala Gly His Leu
 145 150 155 160
Thr Val Ser Phe Tyr Ser Asn
 165

```

&lt;210&gt; SEQ ID NO 138

&lt;211&gt; LENGTH: 384

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Escherichia coli

&lt;400&gt; SEQUENCE: 138

```

Met Asn Lys Ile Leu Phe Ile Phe Thr Leu Phe Phe Ser Ser Gly Phe
 1                               5 10 15
Phe Thr Phe Ala Val Ser Ala Asp Lys Asn Pro Gly Ser Glu Asn Met
 20 25 30
Thr Asn Thr Ile Gly Pro His Asp Arg Gly Gly Ser Ser Pro Ile Tyr
 35 40 45

```

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Asn Ile Leu Asn Ser Tyr Leu Thr Ala Tyr Asn Gly Ser His His Leu  
 50 55 60  
 Tyr Asp Arg Met Ser Phe Leu Cys Leu Ser Ser Gln Asn Thr Leu Asn  
 65 70 75 80  
 Gly Ala Cys Pro Ser Ser Asp Ala Pro Gly Thr Ala Thr Ile Asp Gly  
 85 90 95  
 Glu Thr Asn Ile Thr Leu Gln Phe Thr Glu Lys Arg Ser Leu Ile Lys  
 100 105 110  
 Arg Glu Leu Gln Ile Lys Gly Tyr Lys Gln Phe Leu Phe Lys Asn Ala  
 115 120 125  
 Asn Cys Pro Ser Lys Leu Ala Leu Asn Ser Ser His Phe Gln Cys Asn  
 130 135 140  
 Arg Glu Gln Ala Ser Gly Ala Thr Leu Ser Leu Tyr Ile Pro Ala Gly  
 145 150 155 160  
 Glu Leu Asn Lys Leu Pro Phe Gly Gly Val Trp Asn Ala Val Leu Lys  
 165 170 175  
 Leu Asn Val Lys Arg Arg Tyr Asp Thr Thr Tyr Gly Thr Tyr Thr Ile  
 180 185 190  
 Asn Ile Thr Val Asn Leu Thr Asp Lys Gly Asn Ile Gln Ile Trp Leu  
 195 200 205  
 Pro Gln Phe Lys Ser Asn Ala Arg Val Asp Leu Asn Leu Arg Pro Thr  
 210 215 220  
 Gly Gly Gly Thr Tyr Ile Gly Arg Asn Ser Val Asp Met Cys Phe Tyr  
 225 230 235 240  
 Asp Gly Tyr Ser Thr Asn Ser Ser Ser Leu Glu Ile Arg Phe Gln Asp  
 245 250 255  
 Asp Asn Ser Lys Ser Asp Gly Lys Phe Tyr Leu Lys Lys Ile Asn Asp  
 260 265 270  
 Asp Ser Lys Glu Leu Val Tyr Thr Leu Ser Leu Leu Leu Ala Gly Lys  
 275 280 285  
 Asn Leu Thr Pro Thr Asn Gly Gln Ala Leu Asn Ile Asn Thr Ala Ser  
 290 295 300  
 Leu Glu Thr Asn Trp Asn Arg Ile Thr Ala Val Thr Met Pro Glu Ile  
 305 310 315 320  
 Ser Val Pro Val Leu Cys Trp Pro Gly Arg Leu Gln Leu Asp Ala Lys  
 325 330 335  
 Val Lys Asn Pro Glu Ala Gly Gln Tyr Met Gly Asn Ile Lys Ile Thr  
 340 345 350  
 Phe Thr Pro Ser Ser Gln Thr Leu Asp Asn Lys Gln Val Glu Lys Asn  
 355 360 365  
 Ile Thr Val Thr Ala Ser Val Asp Pro Ala Ile Asp Leu Leu Gln Ala  
 370 375 380

<210> SEQ ID NO 139  
 <211> LENGTH: 1002  
 <212> TYPE: DNA  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 139

atgaataaaa ttttatttat ttttacattg ttttttctt cagggttttt tacatttgcc 60  
 gtatcgccag ataaaaatcc cggaagtgaa aacatgacta atactattgg tccccatgac 120  
 aggggggat cttccccat atataatc ttaaattcct atcttacagc atacaatgga 180  
 agccatcatc tgtatgatag gatgagtttt ttatgtttgt cttctcaaaa tacactgaat 240

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ggagcatgcc caagcagtga tgcccctggc actgctacaa ttgatggcga aacaaatata 300
acattacaat ttacggaaaa aagaagtcta attaaaagag aactgcaaat taaaggctat 360
aaacaatttt tgttcaaaaa tgctaattgc ccatctaac tagcacttaa ctcatctcat 420
tttcaatgta atagagaaca agcttcaggt gctactttat cgttatacat accagctggt 480
gaattaaata aattaccttt tggggggggtc tggaatgccg ttctgaagct aaatgtaaaa 540
agacgatatg atacaaccta tgggacttac actataaaca tcacagtaa tttactgat 600
aagggaata ttcagatag gttaccacag ttcaaaagta acgctcgtgt cgatcttaac 660
ttgctccaa ctggtggtgg tacatatatc ggaagaaatt ctgttgatag gtgctttat 720
gatggatata gtactaacag cagctcttta gagataagat ttcaggatga taattctaaa 780
tctgatggaa aattttatct aaagaaaata aatgatgact ccaaagaact tgtatacact 840
ttgtcacttc tcctggcagg taaaaattha acaccaacaa atggacaggc attaaatatt 900
aacactgctt ctctggaac aaactggaat agaattacag ctgtcaccat gccagaaatc 960
agtgttccgg tgttgtgttg gctggacgt ttgcaattgg at 1002

```

&lt;210&gt; SEQ ID NO 140

&lt;211&gt; LENGTH: 1629

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Escherichia coli

&lt;400&gt; SEQUENCE: 140

```

atgaataaaa ttttatttat ttttacattg ttttttctt cagggttttt tacatttgcc 60
gtatcggcag ataaaaatcc cggaaagtga aacatgacta atactattgg tcccatgac 120
aggggggat cttccccc atataatata ttaaattcct atcttacagc atacaatgga 180
agccatcatc tgtatgatag gatgagtttt ttatgtttgt cttctcaaaa tacactgaat 240
ggagcatgcc caagcagtga tgcccctggc actgctacaa ttgatggcga aacaaatata 300
acattacaat ttacggaaaa aagaagtcta attaaaagag aactgcaaat taaaggctat 360
aaacaatttt tgttcaaaaa tgctaattgc ccatctaac tagcacttaa ctcatctcat 420
tttcaatgta atagagaaca agcttcaggt gctactttat cgttatacat accagctggt 480
gaattaaata aattaccttt tggggggggtc tggaatgccg ttctgaagct aaatgtaaaa 540
agacgatatg atacaaccta tgggacttac actataaaca tcacagtaa tttactgat 600
aagggaata ttcagatag gttaccacag ttcaaaagta acgctcgtgt cgatcttaac 660
ttgctccaa ctggtggtgg tacatatatc ggaagaaatt ctgttgatag gtgctttat 720
gatggatata gtactaacag cagctcttta gagataagat ttcaggatga taattctaaa 780
tctgatggaa aattttatct aaagaaaata aatgatgact ccaaagaact tgtatacact 840
ttgtcacttc tcctggcagg taaaaattha acaccaacaa atggacaggc attaaatatt 900
aacactgctt ctctggaac aaactggaat agaattacag ctgtcaccat gccagaaatc 960
agtgttccgg tgttgtgttg gctggacgt ttgcaattgg atgcaaaagt gaaaaatccc 1020
gaggctggac aatatatggg gaatattaaa attactttca caccaagtag tcaaacactc 1080
gacaataaac aagtagagaa aaatattact gtaacagcta gtgttgatcc tgcaattgat 1140
cttttgcaag ctgatggcaa tgctctgcca tcagctgtaa agttagetta ttctcccgca 1200
tcaaaaactt ttgaaagtta cagagtaatg actcaagttc atacaaacga tgcaactaaa 1260
aaagtaattg ttaaaactgc tgatacacca cagcttacag atgttctgaa ttaactgtt 1320

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caaatgccta tcagtgtgtc atggggagga caagtattat ctacaacagc caaagaattt 1380
gaagctgctg ctttgggata ttctgcatcc ggtgtaaattg gcgtatcatc ttctcaagag 1440
ttagtaatta gcgctgcacc taaaactgcc ggtaccgccc caactgcagg aaactattca 1500
ggagtagtat ctcttgaat gactttggga tccgacaata aacaagtaga gaaaaatatt 1560
actgtaacag ctagtgttga tcctgtgatt gatcttttgc aactcgagca ccaccaccac 1620
caccactga 1629

```

&lt;210&gt; SEQ ID NO 141

&lt;211&gt; LENGTH: 542

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Escherichia coli

&lt;400&gt; SEQUENCE: 141

```

Met Asn Lys Ile Leu Phe Ile Phe Thr Leu Phe Phe Ser Ser Gly Phe
1           5           10          15
Phe Thr Phe Ala Val Ser Ala Asp Lys Asn Pro Gly Ser Glu Asn Met
20          25          30
Thr Asn Thr Ile Gly Pro His Asp Arg Gly Gly Ser Ser Pro Ile Tyr
35          40          45
Asn Ile Leu Asn Ser Tyr Leu Thr Ala Tyr Asn Gly Ser His His Leu
50          55          60
Tyr Asp Arg Met Ser Phe Leu Cys Leu Ser Ser Gln Asn Thr Leu Asn
65          70          75          80
Gly Ala Cys Pro Ser Ser Asp Ala Pro Gly Thr Ala Thr Ile Asp Gly
85          90          95
Glu Thr Asn Ile Thr Leu Gln Phe Thr Glu Lys Arg Ser Leu Ile Lys
100         105         110
Arg Glu Leu Gln Ile Lys Gly Tyr Lys Gln Phe Leu Phe Lys Asn Ala
115         120         125
Asn Cys Pro Ser Lys Leu Ala Leu Asn Ser Ser His Phe Gln Cys Asn
130         135         140
Arg Glu Gln Ala Ser Gly Ala Thr Leu Ser Leu Tyr Ile Pro Ala Gly
145         150         155         160
Glu Leu Asn Lys Leu Pro Phe Gly Gly Val Trp Asn Ala Val Leu Lys
165         170         175
Leu Asn Val Lys Arg Arg Tyr Asp Thr Thr Tyr Gly Thr Tyr Thr Ile
180         185         190
Asn Ile Thr Val Asn Leu Thr Asp Lys Gly Asn Ile Gln Ile Trp Leu
195         200         205
Pro Gln Phe Lys Ser Asn Ala Arg Val Asp Leu Asn Leu Arg Pro Thr
210         215         220
Gly Gly Gly Thr Tyr Ile Gly Arg Asn Ser Val Asp Met Cys Phe Tyr
225         230         235         240
Asp Gly Tyr Ser Thr Asn Ser Ser Ser Leu Glu Ile Arg Phe Gln Asp
245         250         255
Asp Asn Ser Lys Ser Asp Gly Lys Phe Tyr Leu Lys Lys Ile Asn Asp
260         265         270
Asp Ser Lys Glu Leu Val Tyr Thr Leu Ser Leu Leu Leu Ala Gly Lys
275         280         285
Asn Leu Thr Pro Thr Asn Gly Gln Ala Leu Asn Ile Asn Thr Ala Ser
290         295         300
Leu Glu Thr Asn Trp Asn Arg Ile Thr Ala Val Thr Met Pro Glu Ile
305         310         315         320

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Ser Val Pro Val Leu Cys Trp Pro Gly Arg Leu Gln Leu Asp Ala Lys  
 325 330 335

Val Lys Asn Pro Glu Ala Gly Gln Tyr Met Gly Asn Ile Lys Ile Thr  
 340 345 350

Phe Thr Pro Ser Ser Gln Thr Leu Asp Asn Lys Gln Val Glu Lys Asn  
 355 360 365

Ile Thr Val Thr Ala Ser Val Asp Pro Ala Ile Asp Leu Leu Gln Ala  
 370 375 380

Asp Gly Asn Ala Leu Pro Ser Ala Val Lys Leu Ala Tyr Ser Pro Ala  
 385 390 395 400

Ser Lys Thr Phe Glu Ser Tyr Arg Val Met Thr Gln Val His Thr Asn  
 405 410 415

Asp Ala Thr Lys Lys Val Ile Val Lys Leu Ala Asp Thr Pro Gln Leu  
 420 425 430

Thr Asp Val Leu Asn Ser Thr Val Gln Met Pro Ile Ser Val Ser Trp  
 435 440 445

Gly Gly Gln Val Leu Ser Thr Thr Ala Lys Glu Phe Glu Ala Ala Ala  
 450 455 460

Leu Gly Tyr Ser Ala Ser Gly Val Asn Gly Val Ser Ser Ser Gln Glu  
 465 470 475 480

Leu Val Ile Ser Ala Ala Pro Lys Thr Ala Gly Thr Ala Pro Thr Ala  
 485 490 495

Gly Asn Tyr Ser Gly Val Val Ser Leu Val Met Thr Leu Gly Ser Asp  
 500 505 510

Asn Lys Gln Val Glu Lys Asn Ile Thr Val Thr Ala Ser Val Asp Pro  
 515 520 525

Val Ile Asp Leu Leu Gln Leu Glu His His His His His His  
 530 535 540

<210> SEQ ID NO 142  
 <211> LENGTH: 1176  
 <212> TYPE: DNA  
 <213> ORGANISM: Escherichia coli

<400> SEQUENCE: 142

atgaataaaa ttttatttat ttttacattg tttttttcct cagggttttt tacatttgcc 60

gtatcggcag ataaaaatcc cggaagtga aacatgacta atactattgg tccccatgac 120

aggggggggat cttcccccat atataatc ttaaattcct atcttacagc atacaatgga 180

agccatcatc tgtatgatag gatgagtttt ttatgtttgt cttctcaaaa taaactgaat 240

ggagcatgcc caagcagtga tgcccctggc actgctacaa ttgatggcga aacaaatata 300

acattacaat ttacggaaaa aagaagtcta attaaaagag aactgcaaat taaaggctat 360

aaacaatttt tgttcaaaaa tgctaattgc ccatctaac tagcacttaa ctcatctcat 420

tttcaatgta atagagaaca agcttcaggt gctactttat cgttatacat accagctggt 480

gaattaaata aattacccttt tggggggggtc tggaatgccc ttctgaagct aaatgtaaaa 540

agacgatatg atacaacctt tgggacttac actataaaca tcacagttaa ttttaactgat 600

aagggaaata ttcagatgat gttaccacag ttcaaaagta acgctcgtgt cgatcttaac 660

ttgctgctcaa ctgggtggtgg tacatatatc ggaagaaatt ctgttgatat gtgcttttat 720

gatggatata gtactaacag cagctcttta gagataagat ttcaggatga taattctaaa 780

tctgatggaa aattttatct aaagaaaata aatgatgact ccaaagaact tgtatacact 840

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ttgtcacttc tcctggcagg taaaaattta acaccaacaa atggacaggc attaaatatt    900
aacactgctt ctctggaac aaactggaat agaattacag ctgtcaccat gccagaaatc    960
agtgttccgg tgttgtggtt goctggacgt ttgcaattgg atgcaaaagt gaaaaatccc    1020
gaggctggac aatatatggg gaatattaaa attactttca caccaagtag tcaaactctc    1080
gacaataaac aagtagagaa aaatattact gtaacagcta gtgttgatcc tgtgattgat    1140
cttttgaac tcgagcacca ccaccaccac cactga                                1176
    
```

```

<210> SEQ ID NO 143
<211> LENGTH: 391
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli
    
```

<400> SEQUENCE: 143

```

Met Asn Lys Ile Leu Phe Ile Phe Thr Leu Phe Phe Ser Ser Gly Phe
1           5           10          15
Phe Thr Phe Ala Val Ser Ala Asp Lys Asn Pro Gly Ser Glu Asn Met
20          25          30
Thr Asn Thr Ile Gly Pro His Asp Arg Gly Gly Ser Ser Pro Ile Tyr
35          40          45
Asn Ile Leu Asn Ser Tyr Leu Thr Ala Tyr Asn Gly Ser His His Leu
50          55          60
Tyr Asp Arg Met Ser Phe Leu Cys Leu Ser Ser Gln Asn Thr Leu Asn
65          70          75          80
Gly Ala Cys Pro Ser Ser Asp Ala Pro Gly Thr Ala Thr Ile Asp Gly
85          90          95
Glu Thr Asn Ile Thr Leu Gln Phe Thr Glu Lys Arg Ser Leu Ile Lys
100         105         110
Arg Glu Leu Gln Ile Lys Gly Tyr Lys Gln Phe Leu Phe Lys Asn Ala
115         120         125
Asn Cys Pro Ser Lys Leu Ala Leu Asn Ser Ser His Phe Gln Cys Asn
130         135         140
Arg Glu Gln Ala Ser Gly Ala Thr Leu Ser Leu Tyr Ile Pro Ala Gly
145         150         155         160
Glu Leu Asn Lys Leu Pro Phe Gly Gly Val Trp Asn Ala Val Leu Lys
165         170         175
Leu Asn Val Lys Arg Arg Tyr Asp Thr Thr Tyr Gly Thr Tyr Thr Ile
180         185         190
Asn Ile Thr Val Asn Leu Thr Asp Lys Gly Asn Ile Gln Ile Trp Leu
195         200         205
Pro Gln Phe Lys Ser Asn Ala Arg Val Asp Leu Asn Leu Arg Pro Thr
210         215         220
Gly Gly Gly Thr Tyr Ile Gly Arg Asn Ser Val Asp Met Cys Phe Tyr
225         230         235         240
Asp Gly Tyr Ser Thr Asn Ser Ser Ser Leu Glu Ile Arg Phe Gln Asp
245         250         255
Asp Asn Ser Lys Ser Asp Gly Lys Phe Tyr Leu Lys Lys Ile Asn Asp
260         265         270
Asp Ser Lys Glu Leu Val Tyr Thr Leu Ser Leu Leu Leu Ala Gly Lys
275         280         285
Asn Leu Thr Pro Thr Asn Gly Gln Ala Leu Asn Ile Asn Thr Ala Ser
290         295         300
Leu Glu Thr Asn Trp Asn Arg Ile Thr Ala Val Thr Met Pro Glu Ile
305         310         315         320
    
```

-continued

Ser Val Pro Val Leu Cys Trp Pro Gly Arg Leu Gln Leu Asp Ala Lys  
 325 330 335

Val Lys Asn Pro Glu Ala Gly Gln Tyr Met Gly Asn Ile Lys Ile Thr  
 340 345 350

Phe Thr Pro Ser Ser Gln Thr Leu Asp Asn Lys Gln Val Glu Lys Asn  
 355 360 365

Ile Thr Val Thr Ala Ser Val Asp Pro Val Ile Asp Leu Leu Gln Leu  
 370 375 380

Glu His His His His His His  
 385 390

What is claimed is:

1. A multi-agent immunogenic construct, comprising a *Campylobacter jejuni* capsule polysaccharide conjugated to a protein carrier, wherein said protein carrier comprises an *Escherichia coli* enterotoxigenic recombinant polypeptide construct, wherein said *Escherichia coli* recombinant polypeptide construct comprises a minor or major subunit connected to one or more major fimbrial subunits or immunogenic fragments, thereof, of the same fimbrial type, via a polypeptide linker, are also connected to each other via a polypeptide linker wherein the C-terminal *Escherichia coli* fimbrial major subunit is connected, via a linker, to a C-terminal donor  $\beta$  strand derived from a major *Escherichia coli* fimbrial subunit that is homologous or heterologous to the immediately N-terminal major subunit, wherein said donor  $\beta$  strand contains 12 to 16 amino acids from the N-terminal region of said one or more major fimbrial subunits, and wherein said recombinant polypeptide construct can be connected to one or more additional recombinant polypeptide constructs, wherein each of the constructs contain fimbrial subunits derived from a different fimbrial type than any of the other constructs and wherein the recombinant polypeptide construct can contain a C-terminal histidine tag at the C-terminus, wherein said minor or major *Escherichia coli* fimbrial subunits are derived from ETEC strains selected from the group consisting of Class 5, CS3 and CS6.

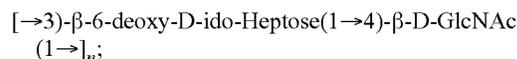
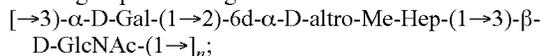
2. The multi-agent immunogenic construct of claim 1, wherein the multi-agent immunogenic construct comprises *Shigella* lipopolysaccharide in place of or in addition to the *Campylobacter jejuni* capsule polysaccharide.

3. The multi-agent immunogenic construct of claim 1, wherein said molar ratio of *Campylobacter jejuni* or *Shigella* spp. lipopolysaccharide to *Escherichia coli* recombinant protein carrier is 1:1 to 5:1.

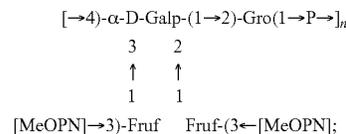
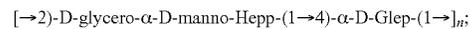
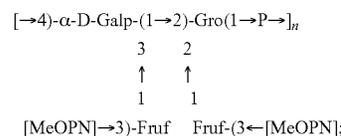
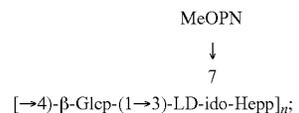
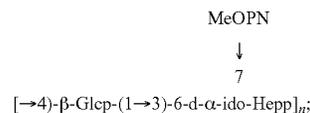
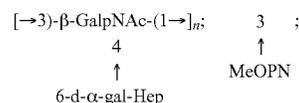
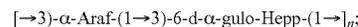
4. The multi-agent immunogenic construct of claim 1, wherein the *Escherichia coli* recombinant polypeptide construct comprises the amino acid sequence selected from the group consisting of SEQ ID Nos. 108 and 110.

5. The multi-agent immunogenic construct of claim 1, wherein the *Escherichia coli* recombinant polypeptide construct is encoded by the nucleotide sequence of SEQ ID Nos. 105 and 109.

6. The multi-agent immunogenic construct of claim 1, wherein said *Campylobacter jejuni* polysaccharide is a repeating trisaccharide structure having the formula selected from the group consisting of:



selected from the group consisting of:

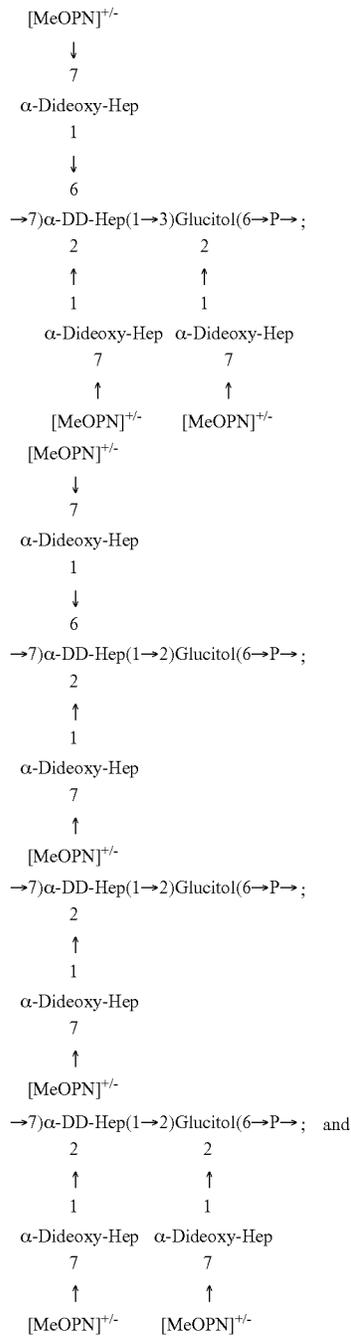


$[\rightarrow 3)-L-beta-ido-Hep-(1 \rightarrow 4)-beta-D-Glc-(1 \rightarrow)_n$ , with non-stoichiometric substitution of O-methyl-phosphoramidate at position 2 of L-glycero-beta-D-ido-heptose;

$[\rightarrow 3)-6d-beta-ido-Hep-(1 \rightarrow 4)-beta-D-Glc-(1 \rightarrow)_n$ , derived from HS13, with non-stoichiometric substitution of O-methyl-phosphoramidate at position 2 or/and 7 of 6-deoxy-beta-D-ido-heptose;

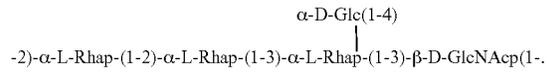
$[\rightarrow 3)-L-beta-D-ido-Hep-(1 \rightarrow 4)-beta-D-Glc-(1 \rightarrow)_n$ ;

$[\rightarrow 3)-L-alpha-D-ido-Hep-(1 \rightarrow 4)-alpha-Gal-(1 \rightarrow)_n$ , with non-stoichiometric substitution of O-methyl-phosphoramidate at position 2 of 6-deoxy-alpha-D-ido-heptose;



[→3)-6d-alpha-D-ido-Hep-(1→4)-alpha-Gal-(1→)<sub>n</sub>, derived from HS3, HS13 and HS50 with non-stoichiometric substitution of O-methyl-phosphoramidate at position 2 of L-glycero-alpha-D-ido-heptose, wherein "n" is 1 to 100.

7. The multi-agent immunogenic construct of claim 2, wherein said *Shigella* lipopolysaccharide has the structure:



5 8. The multi-agent immunogenic construct of claim 1, wherein said N-terminus of said minor or major subunit contains an 18-22 amino acid signal peptide.

9. The multi-agent immunogenic construct of claim 1, wherein the amino acid sequence of said polypeptide linker is the amino acid sequence of SEQ ID No. 5 or a tri-glycine.

10 10. The multi-agent immunogenic construct of claim 1, wherein one or more major subunits contain a deletion of the 14 to 18 N-terminal amino acids.

11. The multi-agent Immunogenic construct of claim 1, wherein said amino acid sequence of said *Escherichia coli* fimbrial minor subunit is selected from the group consisting of SEQ ID Nos. 46, 52 and 58, or derivatives thereof, and wherein said amino acid sequence of said *Escherichia coli* fimbrial major subunit is selected from the group consisting of SEQ ID Nos. 55 and 61, or derivatives thereof.

12. A method of inducing an immune response against *C. jejuni* strains, wherein said method induces an immune response against one or more enterobacteria selected from the group consisting of *C. jejuni* strains, *Escherichia coli*, and *Shigella*, comprising the steps: a. administering the multi-agent immunogenic composition of claim 1 at a dose range of 0.1 μg to 10 mg per dose; b. administering a boosting dose of said capsule polysaccharide composition as in section a) at a dose range of 0.1 μg to 10 mg per dose.

13. The method of claim 12, wherein said *Campylobacter jejuni* capsule polysaccharide comprises the polysaccharide structures of claim 6.

14. The method of claim 12, wherein said multi-agent immunogenic composition comprises the construct of claim 2.

15. The method of claim 12, wherein said *Escherichia coli* enterotoxigenic recombinant polypeptide construct wherein said *Escherichia coli* fimbrial minor subunit is selected from the group consisting of SEQ ID Nos. 46 and 58 or derivatives thereof, and wherein said amino acid sequence of said *Escherichia coli* fimbrial major subunit is selected from the group consisting of SEQ ID Nos. 49, 55 and 61, or derivatives thereof.

16. The method of claim 12, wherein the *Escherichia coli* recombinant polypeptide construct comprises the amino acid sequence selected from the group consisting of SEQ ID Nos. 108 and 110.

17. The method of claim 12, wherein the *Escherichia coli* recombinant polypeptide construct is encoded by the nucleotide sequence of SEQ ID Nos. 105 and 109.

18. The method of claim 12, wherein said N-terminus of said minor or major subunit contains an 18-22 amino acid signal peptide.

19. The method of claim 12, wherein the amino acid sequence of said polypeptide linker is the amino acid sequence of SEQ ID No. 5 or a tri-glycine.

20. The method of claim 12, wherein one or more major subunits contain a deletion of the 14 to 18 N-terminal amino acids.

\* \* \* \* \*